

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:17:16 ; Search time 44 seconds  
(without alignments)  
415.126 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNNGYFYSYVND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	2 S39154	xylanase 1 - fungu
2	1045	100.0	223	2 S39883	endo-1,4-beta-xyla
3	1022	97.8	190	1 A44594	endo-1,4-beta-xyla
4	1005	96.2	190	1 A44595	endo-1,4-beta-xyla
5	996	95.3	190	1 A44593	endo-1,4-beta-xyla
6	765.5	73.3	241	2 S71473	endo-1,4-beta-xyla
7	705.5	67.5	219	2 S71472	endo-1,4-beta-xyla
8	701.5	67.1	232	2 JC7577	endo-1,4-beta-xyla
9	684.5	65.5	225	1 S57477	endo-1,4-beta-xyla
10	670.5	64.2	221	1 S57469	endo-1,4-beta-xyla
11	656	62.8	221	2 JC7307	endo-1,4-beta-xyla
12	614.5	58.8	227	2 S43919	endo-1,4-beta-xyla
13	591	56.6	333	1 JS0590	endo-1,4-beta-xyla
14	591	56.6	335	2 T50601	endo-1,4-beta-xyla
15	575.5	55.1	644	1 I40712	endo-1,4-beta-xyla
16	565.5	54.1	197	1 A44597	endo-1,4-beta-xyla
17	536.5	51.3	661	1 S59633	endo-1,4-beta-xyla
18	530.5	50.8	241	2 T37005	endo-1,4-beta-xyla
19	527	50.4	240	1 JS0591	endo-1,4-beta-xyla
20	526.5	50.4	656	1 S59631	endo-1,4-beta-xyla
21	525	50.2	240	1 S47512	endo-1,4-beta-xyla
22	524.5	50.2	210	2 C83762	endo-1,4-beta-xyla
23	503	48.1	213	1 I40569	endo-1,4-beta-xyla
24	502	48.0	213	1 S01734	endo-1,4-beta-xyla
25	502	48.0	213	1 S48126	endo-1,4-beta-xyla
26	468	44.8	354	1 S51779	endo-1,4-beta-xyla
27	462	44.2	228	1 WBSXP	endo-1,4-beta-xyla
28	453.5	43.4	261	1 S12745	endo-1,4-beta-xyla
29	444	42.5	511	1 JQ1935	endo-1,4-beta-xyla

xylanase 2 - fungu  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
xylanase, beta(1,3  
XynB precursor - R  
endo-xylanase - rum  
endo-1,4-beta-xyla  
xylanase (EC 3.2.1  
endo-1,4-beta-xyla  
endo-1,4-beta-xyla  
probable ppe prote  
uncharacterized pr

ALIGNMENTS

RESULT 1

S39154

xylanase 1 - fungus (Trichoderma reesei)

C:Species: Trichoderma reesei

C:Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 22-Jun-1999

C:Accession: S39154

R:Toerrien, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; K

Biotechnology 10, 1461-1465, 1992

A:Title: The two major xylanases from trichoderma reesei: characterization of both en

A:Reference number: S39154

A:Accession: S39154

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <TO>

A:Cross-references: EMBL:X69573; NID:g396563; PIDN:CAA49293.1; >ID:g396564

C:Genetics:

A:Gene: xynl

A:Introns: 90/2

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

F;44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match 100.0%; Score 1045; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 7.2e-73;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QTIQPGTGYNNGYFYSYVNDGCHGGVYTNPGGQFVSNNNSGNFVGGKGPCTKKNVI 60

Db 33 QTIQPGTGYNNGYFYSYVNDGCHGGVYTNPGGQFVSNNNSGNFVGGKGPCTKKNVI 92

Qy 61 NFSGSNPNNGNSYLSVYVWNSRNPLIEYIVENFNGTNPSTGATKLGEVTSQSVYDIYRT 120

Db 93 NFSGSNPNNGNSYLSVYVWNSRNPLIEYIVENFNGTNPSTGATKLGEVTSQSVYDIYRT 152

Qy 121 QRVNQPSTIGTATFYQVWNSRRNHRSSGSVNTANHFNAWAQOGLTLPMDYQIVAVEGYF 180

Db 153 QRVNQPSTIGTATFYQVWNSRRNHRSSGSVNTANHFNAWAQOGLTLPMDYQIVAVEGYF 212

Qy 181 SSGSASITVS 190

Db 213 SSGSASITVS 222

RESULT 2

S39883

endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)

N:Alternate names: endoxylanase II

C:Species: Trichoderma reesei

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 22-Jun-1999

C:Accession: S39883; S39884

R:Saarelainen, R.; Paloneimo, M.; Fagerstrom, R.; Suominen, P.L.; Nevalainen, K.M.H.

Mol. Gen. Genet. 241, 497-503, 1993

A:Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxy

A:Reference number: S39883; MUID:94088442; PMID:8264524

A:Accession: S39883

A:Molecule type: DNA

A:Residues: 1-223 <SAA>

A:Cross-references: EMBL:S67387; NID:9455906; PIDN:AAB29346.1; PID:9455907

A:Experimental source: strain QM6a

A:Accession: S39884

A:Molecule type: protein

A:Residues: 34-43;49-57;121-151;178-191 <SAF>

C:Genetics:

A:Gene: xln2

A:Introns: 91/2

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-33/Domain: propeptide #status predicted <PRO>

F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>

F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>

F:71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:110,121/Binding site: substrate (Tyr) #status predicted

F:119,210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.2e-73;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 60

Db 34 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 93

QY 61 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

Db 94 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 153

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180

Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190

Db 214 SSGSASITVS 223

RESULT 3

A44594

endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)

N:Alternate names: xylanase IIA

C:Species: Trichoderma viride

C:Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997

C:Accession: A44594

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44594

A:Molecule type: protein

A:Residues: 1-190 <YAG>

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F:77,88/Binding site: substrate (Tyr) #status predicted

F:86,177/Active site: Glu #status predicted

Query Match

Best Local Similarity 97.8%; Score 1022; DB 1; Length 190;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 50

Db 1 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

Db 61 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 4

A44595

endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma

N:Alternate names: xylanase IIB

C:Species: Trichoderma viride

C:Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998

C:Accession: A44595

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44595

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-190 <YAG>

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F:86,177/Active site: Glu #status predicted

F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted

F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match

Best Local Similarity 96.2%; Score 1005; DB 1; Length 190;

Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 60

Db 1 QTIGPCTGYNNGYFYSYNDGHHGVYTTNGPGQFSVNMNSNGNFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

Db 61 NFSGSYNPNNGNSLSYVGSNRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 5

A44593

endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (str

N:Alternate names: xylanase

C:Species: Trichoderma harzianum

C:Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000

C:Accession: A44593

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44593

A:Molecule type: protein

A;Residues: 1-190 <YAG>

A;Experimental source: strain E58

R;Campbell, R.L.; Rose, D.R.

submitted to the Brookhaven Protein Data Bank, June 1994

A;Reference number: A52868; PDB:1XND

A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190

C;Function:

A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A;Pathway: xylan degradation

C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F;86,177/Active site: Glu #status experimental

Query Match 95.3%; Score 996; DB 1; Length 190;

Best Local Similarity 94.7%; Pred. No. 3.3e-69;

Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTTQPTGTYNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVI 60

DB 1 QTTQPTGTYNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNGNSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

DB 61 NFSGSYNPNGNSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120

QY 121 QRYNQPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYF 180

DB 121 QRYNQPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYF 180

QY 181 SSGSASITVS 190

DB 181 SSGSASITVS 190

RESULT 6

S71473

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile

C;Species: Chaetomium gracile

C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000

C;Accession: S71473; S78207

R;Yoshino, S.; Olshi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.

Curr. Genet. 29, 73-80, 1995

A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus oryzae

A;Reference number: S71472; MUID:96118924; PMID:8595661

A;Accession: S71473

A;Molecule type: DNA

A;Residues: 1-241 <YOS>

A;Cross-references: EMBL:D49851; NID:g1339859; PIDN:BAA08650.1; PID:g1339860

A;Accession: S78207

A;Molecule type: protein

A;Residues: 38-44;89-91;153-161 <YOH>

C;Genetics:

A;Introns: 88/2

C;Function:

A;Pathway: xylan degradation

C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>

F;43-220/Domain: endo-1,4-beta-xylanase homology <XYL>

F;116,207/Active site: Glu #status predicted

Query Match

Best Local Similarity 73.8%; Score 765.5; DB 2; Length 241;

Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVINFGSGY 66

DB 38 TGYNNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVINFGSGY 66

QY 67 NPNNGSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTQVNOP 126

DB 67 NPNNGSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTQVNOP 126

DB 97 NPNNGSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTQVNOP 156

QY 127 SIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYFSSGSAS 186

DB 157 SIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYFSSGSAT 216

QY 187 ITV 189

DB 217 VNV 219

RESULT 7

S71472

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile

N;Alternate names: xylanase A

C;Species: Chaetomium gracile

C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000

C;Accession: S71472; S78206

R;Yoshino, S.; Olshi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.

Curr. Genet. 29, 73-80, 1995

A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus oryzae

A;Reference number: S71472; MUID:96118924; PMID:8595661

A;Accession: S71472

A;Molecule type: DNA

A;Residues: 1-219 <YOS>

A;Cross-references: EMBL:D49850; NID:g1339857; PIDN:BAA08649.1; PID:g1339858

A;Accession: S78206

A;Molecule type: protein

A;Residues: 31-45;82-94;152-160 <YOH>

C;Genetics:

A;Introns: 81/2

C;Function:

A;Pathway: xylan degradation

C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>

F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>

F;115,206/Active site: Glu #status predicted

Query Match

Best Local Similarity 67.5%; Score 705.5; DB 2; Length 219;

Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTCYNNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVINFGSGS 65

DB 36 GTCYNNGYFYSYWNDGCGVYTYTNGPGQFQSVNWSNNGFVGGKQWPGTKNKVINFGSGT 94

QY 66 YNPNGNSYLSYVWNSRNPFLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTQVNOP 125

DB 95 FSPQNGYLAITYGWTQNPFLVEYIVESFGTYDPSQASKFGTIQDQGSTVYIAKTRVNO 154

QY 126 PSTIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYFSSGS 185

DB 155 PSIEGTSTFDQFVSRQNRHSSGVSNTANHFNAWAQOGLTLGTMQYQIVAVEGYFSSGS 214

QY 186 SITVS 190

DB 215 SITVS 219

RESULT 8

JC7577

endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae

N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2

C;Species: Aspergillus oryzae

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001

C;Accession: JC7577; PC7120

R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sak

Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000

A;Title: Molecular cloning, overexpression, and purification of a major xylanase from Aspergillus oryzae

A;Reference number: JC7577; MUID: 21077500; PMID:11210150

A;Accession: JC7577

A:Molecule type: DNA  
A:Residues: 1-232 <KIM>

A:Cross-References: DDBJ:AB044941

A:Experimental source: strain KBN616

A:Accession: PC7120

A:Molecule type: protein

A:Residues: 45-64 <K12>

C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de

C:Genetics:

A:Gene: xynG2

A:Introns: 100/2

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase

Query Match 67.1%; Score 701.5; DB 2; Length 232;

Best Local Similarity 67.8%; Pred. No. 1.3e-46;

Matches 124; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

QY 7 TCYNGYFYSYNDGGVYTYNGPGQFVSVMNSGNGFVGGKQWPGTKNKNVNFSGSY 66

DB 50 TCYNGYFYSYNDGGVYTYNGPGQFVSVMNSGNGFVGGKQWPGTKNKNVNFSGSY 108

QY 67 NPNGNSYLSVYGWSRNPLEYIVENFGYINPSTGATKLGVEVTSQGVVDIYRTORVNOP 126

DB 109 NPNGNSYLSVYGWSRNPLEYIVENFGYINPSTGATKLGVEVTSQGVVDIYRTORVNAP 168

QY 127 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 186

DB 169 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 228

QY 187 ITV 189

DB 229 ITV 231

RESULT 9

S57477

endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans

N:Alternate names: xylanase 1

C:Species: Emericella nidulans, Aspergillus nidulans

C:Date: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 23-Mar-2001

C:Accession: S57477

R:Perez-Gonzalez, J.A.

submitted to the EMBL Data Library, June 1995

A:Description: Expression in Saccharomyces cerevisiae of two, xylanase encoding genes fro

A:Reference number: S57469

A:Accession: S57477

A:Molecule type: DNA

A:Residues: 1-225 <PER>

A:Cross-References: EMBL:Z49892; NID:9870832; PIDN:CAA90073.1; PID:9870833

C:Genetics:

A:Introns: 93/2

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>

F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>

F:121,212/Active site: Glu #status predicted

Query Match 65.5%; Score 684.5; DB 1; Length 225;

Best Local Similarity 66.1%; Pred. No. 2.5e-45;

Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 TCYNGYFYSYNDGGVYTYNGPGQFVSVMNSGNGFVGGKQWPGTKNKNVNFSGSY 66

DB 43 TCWSNGYFYSYNDGGVYTYNGAGGSYTVQWSNVGNFVGGKQWPGTKNKNVNFSGSY 101

QY 67 NPNGNSYLSVYGWSRNPLEYIVENFGYINPSTGATKLGVEVTSQGVVDIYRTORVNOP 126

DB 102 NPNGNSYLSVYGWSRNPLEYIVENFGYINPSTGATKLGVEVTSQGVVDIYRTORVNAP 161

QY 127 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 186

DB 162 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 221

QY 187 ITV 189

DB 222 ITV 224

RESULT 10

S57469

endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans

N:Alternate names: xylanase 2

C:Species: Emericella nidulans, Aspergillus nidulans

C:Date: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 08-May-1998

C:Accession: S57469

R:Perez-Gonzalez, J.A.

submitted to the EMBL Data Library, June 1995

A:Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes

A:Reference number: S57469

A:Accession: S57469

A:Molecule type: DNA

A:Residues: 1-221 <PER>

A:Cross-References: EMBL:Z49893; NID:9870834; PID:9870835

C:Genetics:

A:Introns: 89/3

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-19/Domain: signal sequence #status predicted <SIG>

F:19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>

F:44-221/Domain: endo-1,4-beta-xylanase homology <XYL>

F:117,208/Active site: Glu #status predicted

Query Match 64.2%; Score 670.5; DB 1; Length 221;

Best Local Similarity 65.8%; Pred. No. 2.8e-44;

Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TCYNGYFYSYNDGGVYTYNGPGQFVSVMNSGNGFVGGKQWPGTKNKNVNFSGSY 66

DB 39 TCYNGYFYSYNDGGVYTYNGPGQFVSVMNSGNGFVGGKQWPGTKNKNVNFSGSY 97

QY 67 NPNGNSYLSVYGWSRNPLEYIVENFGYINPSTGATKLGVEVTSQGVVDIYRTORVNOP 126

DB 98 IPGNGYLSVYGWQNPLEYIVESYGYDNPAGTAGHGTLESQGSTVDIYRTATRENAP 157

QY 127 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 186

DB 158 SIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYFSSGSAS 217

QY 187 ITVS 190

DB 218 ITVS 221

RESULT 11

JC7307

endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp.

N:Alternate names: endo-1,3-beta-xylanase; xylanase

C:Species: Penicillium sp.

C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000

C:Accession: JC7307; PC7086

R:Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Sakka, K.; Ohmi

Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000

A:Title: Purification, characterization, and molecular cloning of acidophilic xylanas

A:Reference number: JC7307

A:Accession: JC7307

A:Molecule type: DNA

A:Residues: 1-221 <KIM>

A:Cross-References: DDBJ:AB035540



Search completed: May 9, 2003, 10:21:30  
Job time : 45 secs

A:Gene: xlnB  
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Query Match 56.6%; Score 591; DB 2; Length 335;  
Best Local Similarity 55.1%; Pred. No. 5.3e-38;  
Matches 109; Conservative 31; Mismatches 42; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDGHHGGVYTNPGGQFVSNWNSGNEFVGKGWQ 52  
DB 36 PGTAQADFTVTTNQEGTNGYYSFWDQGTVMNMNGSGGYSTSRNTGNFVACKGWA 95  
QY 53 PGTAKNVINPFGSYNPNNGSYLSVYGWNRNPLIEYIVENFGYNEPSTGATKLGVTSDG 112  
DB 96 NGR-RTVOYSGSFNPSGNALYLGWTSNPLVEYIVDWMGYRP-TGEYK-GTITS 152  
QY 113 SVYDIYRTORVNOPSTIGTATFYQWYVSRNRHSSGVSNTANHFNAWAOGLTGLTMD-Y 171  
DB 153 GTYDIYKTRVNPSPVEGTRTFDQYWSVQAKRTGTTTGNHFDWARAGMPLGNFSY 212  
QY 172 QIVAVEGYFSSGSASITV 189  
DB 213 MINATEGYQSSGSSSINV 230

RESULT 15

I40712  
endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi  
N:Alternate names: xylanase D  
C:Species: Cellulomonas fimi  
C:Date: 16-Aug-1996 #sequence\_revision 22-Nov-1996 #text\_change 18-Jun-1999  
C:Accession: I40712  
R:Millward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilb  
Mol. Microbiol. 11, 375-382, 1994  
A:Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d  
A:Reference number: I40712; MUID:94224155; PMID:8170399  
A:Accession: I40712  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-644 <RES>  
A:Cross-references: EMBL:X76729; NID:g558176; PIDN:CAA54145.1; PID:g558177  
C:Genetics:  
A:Gene: xynD  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology;  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <WAT>  
F:54-229/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:361-508/Domain: nodB homology <NODB>  
F:126,216/Active site: Glu #status predicted

Query Match 55.1%; Score 575.5; DB 1; Length 644;  
Best Local Similarity 55.7%; Pred. No. 1.7e-36;  
Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGYNNGYFYSYNDGHHGGVYTNPGGQFVSNWNSGNEFVGKGWQPTKKNKVINFSGSY 66  
DB 49 TGTGDCGYFYSFWDSPGSVMDLNSGGYT-RMSNTGNFVACKGWSGTGR-KTVSYSGQF 106  
QY 67 NPNGNSYLSVYGWNRNPLIEYIVENFGYNEPSTGATKLGVTSDGSVDYDITQRVNOP 126  
DB 107 NPSRNAYLTLYGWTSPLVEYIVDSWGYRPT--GTFMGTVTSDGTYDIYRTQRVNKP 164  
QY 127 SIIG-TATFYQWYVSRNRHSSGVSNTANHFNAWAOGLTGLTMDYQIVAVEGYFSSGSA 185  
DB 165 STGEDSTFYQWYVSRNRHSSGVSNTANHFNAWAOGLTGLTMDYQIVAVEGYFSSGSA 224  
QY 186 SITVS 190  
DB 225 SITVS 229

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:11:31 ; Search time 51 Seconds  
(without alignments)  
342.841 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGFYSYWND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	685	65.6	313	9	US-10-213-990-72
2	675.5	64.6	234	9	US-10-213-990-69
3	669.5	64.1	221	9	US-10-213-990-66
4	647	61.9	217	9	US-09-790-070A-11
5	635.5	60.8	225	9	US-09-467-368-2
6	595.5	57.0	344	10	US-09-770-621-2
7	481.5	46.1	133	9	US-09-790-070A-10
8	470	45.0	221	10	US-09-909-207-3
9	470	45.0	248	10	US-09-909-207-6
10	433	41.4	185	9	US-09-970-616-2
11	177	16.9	84	9	US-09-790-070A-9
12	107.5	10.3	943	9	US-09-996-634-131
13	107.5	10.3	943	9	US-09-997-181-131
14	107.5	10.3	943	9	US-09-997-182-131
15	105	10.0	251	9	US-09-880-748-1554
16	103	9.9	250	9	US-09-880-748-1632
17	92.5	8.9	251	9	US-09-880-748-1185
18	92.5	8.9	255	9	US-09-880-748-841
19	89.5	8.6	256	9	US-09-880-748-1607

20	89	8.5	250	9	US-09-880-748-883	Sequence 883, Ap
21	89	8.5	251	9	US-09-880-748-1512	Sequence 1512, Ap
22	88.5	8.5	253	9	US-09-880-748-1339	Sequence 1339, Ap
23	88.5	8.5	254	9	US-09-880-748-1087	Sequence 1087, Ap
24	88.5	8.5	1109	9	US-09-291-417-88	Sequence 88, Appl
25	88	8.4	218	10	US-09-925-300-1671	Sequence 1671, Ap
26	88	8.4	256	9	US-09-880-748-1285	Sequence 1285, Ap
27	88	8.4	353	9	US-09-935-642-14	Sequence 14, Appl
28	87.5	8.4	477	10	US-09-815-242-13881	Sequence 13881, A
29	87	8.3	251	9	US-09-880-748-1562	Sequence 1562, Ap
30	87	8.3	251	9	US-09-880-748-1586	Sequence 1586, Ap
31	87	8.3	251	9	US-09-880-748-1736	Sequence 1736, Ap
32	87	8.3	251	9	US-09-880-748-1869	Sequence 1869, Ap
33	87	8.3	251	9	US-09-880-748-1870	Sequence 1870, Ap
34	87	8.3	251	9	US-09-880-748-1872	Sequence 1872, Ap
35	87	8.3	251	9	US-09-880-748-1878	Sequence 1878, Ap
36	87	8.3	441	9	US-09-916-494A-10	Sequence 10, Appl
37	86.5	8.3	249	9	US-09-880-748-1618	Sequence 1618, Ap
38	86.5	8.3	378	10	US-09-849-967A-2	Sequence 2, Appl
39	86.5	8.3	479	10	US-09-815-242-10288	Sequence 10288, A
40	86.5	8.3	729	10	US-09-815-242-10132	Sequence 10132, A
41	86	8.2	452	1	US-08-841-636A-35	Sequence 35, Appl
42	85.5	8.2	354	9	US-09-820-843A-21	Sequence 21, Appl
43	85.5	8.2	878	10	US-09-912-020-364	Sequence 364, App
44	85	8.1	333	9	US-10-059-261-61	Sequence 61, Appl
45	84.5	8.1	252	9	US-09-880-748-1690	Sequence 1690, Ap

#### ALIGNMENTS

RESULT 1  
US-10-213-990-72  
; Sequence 72, Application US/10213990  
; Publication No. US20030082595A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Bo  
; APPLICANT: Bussey, Howard  
; APPLICANT: Storms, Reg  
; APPLICANT: Roemer, Terry  
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL  
; FILE REFERENCE: 10182-019-999  
; CURRENT APPLICATION NUMBER: US/10/213,990  
; CURRENT FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Aspergillus  
US-10-213-990-72

Query Match	65.6%	Score 685;	DB 9;	Length 313;
Best Local Similarity	64.2%;	Pred. No. 2.6e-53;		
Matches 124;	Conservative 29;	Mismatches 36;	Indels 4;	Gaps 3;
Qy	1	QTIQPG-TGYNNGYFYSYWNDGHHGVYTNQPGQFQSVNMS--NSGNFVGSGKHQPGTKN	57	
Db	32	QTITTSQTGNNGYYSFWTNAGSVQYTNAGGGEYSVTWANONGDFTCGKGNPGSDH	91	
Qy	58	KVINFGSYPNPNGLSVYGVWSNRNPLIEYIVENFTYNPSTCATKLGVTSDGSVYDI	117	
Db	92	D-ITFSGSFNPGSNAYLSVYGWTTNPLVEYILENYGSPGSGMTHTKGTVTSFGSTYDI	150	
Qy	118	YRTORVNQPSITGCTATGYOWSVSRNHRSSCSVNTANHFNAOQGLTCTMDYQIVAVE	177	
Db	151	YEHQVQNPISLVGTATNQYMSIRKQNRSGTGTATTANFKAWSLGMLGTHNTYQIVSTE	210	
Qy	178	GYFSSGSASITVS	190	
Db	211	GYESSGTITVS	223	

## RESULT 2

US-10-213-990-69  
; Sequence 69, Application US/10213990  
; Publication No. US20030082595A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Bo  
; APPLICANT: Bussey, Howard  
; APPLICANT: Storms, Reg  
; APPLICANT: Roemer, Terry  
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL  
; FILE REFERENCE: 10182-019-999  
; CURRENT APPLICATION NUMBER: US/10/213,990  
; CURRENT FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Aspergillus  
US-10-213-990-69

Query Match 64.6%; Score 675.5; DB 9; Length 234;  
Best Local Similarity 63.3%; Pred. No. 1.3e-52;  
Matches 119; Conservative 25; Mismatches 39; Indels 5; Gaps 1;  
QY 7 TGYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEVGGKMQPGTK-----NKVIN 61  
DB 46 TGNNGYFYSEFTDGGDYTTNGAGGSYSVMNRNVGNEVGGKWNPGSARYALSRRTIN 105  
QY 62 FGSYNPNNSLSVYGWNRNPLIEYYIVENFGTNPSTGATKLGVEVSDGVSVDIYRTQ 121  
DB 106 YGGSFNPNGSLAVYGTNTNPLIEYYVYESYCTYNPFGSGTFRGVTNDGGTYNYTAV 165  
QY 122 RYNOPSIICTATFYQWSVRNRHRSRGSVNTANHFNAWAQOGLTGTMDYQIVAVEGYFS 181  
DB 166 RYNAPSIETKFTQIWSVRTSKRTGVTMANHFNAWSRLGNLGNLTHNYQIVATEGYOS 225  
QY 182 SGSASITV 189  
DB 226 SGSASITV 233

## RESULT 3

US-10-213-990-66  
; Sequence 66, Application US/10213990  
; Publication No. US20030082595A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Bo  
; APPLICANT: Bussey, Howard  
; APPLICANT: Storms, Reg  
; APPLICANT: Roemer, Terry  
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL  
; FILE REFERENCE: 10182-019-999  
; CURRENT APPLICATION NUMBER: US/10/213,990  
; CURRENT FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Aspergillus  
US-10-213-990-66

Query Match 64.1%; Score 669.5; DB 9; Length 221;  
Best Local Similarity 64.1%; Pred. No. 4.2e-52;  
Matches 118; Conservative 27; Mismatches 38; Indels 1; Gaps 1;  
QY 7 TGYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEVGGKMQPGTKNKNVFNFSGY 66  
DB 39 TGTNNNGYFYSEFTDGGQVYTTNGGQYQVDNNGCGNEVACKGNPASE-KAVTYSGSW, 97

QY 67 NPNGNSYLSVYGWNRNPLIEYYIVENFGTNPSTGATKLGVEVSDGVSVDIYRTQVRNP 126  
DB 98 QTSNGYLSVYGWNTSPFLVEFVIVESYGYDPSGTGATHLCVTESDGTATNLYKTRTNAP 157  
QY 127 SIIGTATFYQWSVRNRHRSRGSVNTANHFNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 186  
DB 158 SIIGTATFYQWSVRTSHRQSGTVTYTKNHFDAWRNAGLQGNFDMIVATEGYQSSGSAT 217  
QY 187 ITVS 190  
DB 218 ITVS 221

## RESULT 4

US-09-790-070A-11  
; Sequence 11, Application US/09790070A  
; Publication No. US20030053999A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonniaux, Jean-Luc  
; APPLICANT: Dauvin, Thierry  
; TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY  
; FILE REFERENCE: VANM199.001AUS  
; CURRENT APPLICATION NUMBER: US/09/790,070A  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: EP 00870028.8  
; PRIOR FILING DATE: 2000-02-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Penicillium griseofulvum  
US-09-790-070A-11

Query Match 61.9%; Score 647; DB 9; Length 217;  
Best Local Similarity 63.6%; Pred. No. 4.1e-50;  
Matches 117; Conservative 26; Mismatches 39; Indels 2; Gaps 2;

QY 8 GYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEVGGKMQPGTKNKNVFNFSGSYN 67  
DB 35 GTNGGYFYSEFTNGGGSVSYNNAGNQYVNMKNCSFTSGKMGATGSARN-INP,SGNFEN 93  
QY 68 PNGNSYLSVYGWNRNPLIEYYIVENFGTNPSTGATKLGVEVSDGVSVDIYRTQVRNP 127  
DB 94 PSGNAYLAVYGTWKGPLVEYIYMENTYGEYNPGSMTFKGTVSDGVSVDIYKHTQVNP 153  
QY 128 IIG-TATFYQWSVRNRHRSRGSVNTANHFNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 186  
DB 154 IISDSTFDQYWSIRKNRSGTVTYTGHNHFNAWAKLGMGLGSHDYQIVWTEGYQSSGSAT 213  
QY 187 ITVS 190  
DB 214 ITVS 217

## RESULT 5

US-09-467-368-2  
; Sequence 2, Application US/09467368  
; Patent No. US20020160080A1  
; GENERAL INFORMATION:  
; APPLICANT: Hansen, Peter Kamp  
; APPLICANT: Wagner, Peter  
; APPLICANT: Mullertz, Anette  
; APPLICANT: Knapp, Inge Helmer  
; TITLE OF INVENTION: Animal Feed Additives  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: No. US20020160080A1 No. US20020160080A1disk of No. US20020201  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA





ORGANISM: Penicillium griseofulvum  
US-09-790-070A-10

Query Match 46.1%; Score 481.5; DB 9; Length 133;  
Best Local Similarity 67.4%; Pred. No. 1.2e-35;  
Matches 89; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 60 INFSGSYNPNGLSVYQWNRNPLIEYIVENFGYINPSTGATKLGVTSDGVSVDIYR 119  
DB 2 INFSGNFSGNAYLAVGWTGKPLVEYIMENYGEYFGSGWTFKGTWTSVDSVYDIYK 61  
QY 120 TORVNQPSIIG-TATFYQWVSRRNHRSSGVSNTANHNAAQOGLTLCMTDYOIIVAVEG 178  
DB 62 HTQVNPQSIISSTFDQWYSIRNRKRSSTVTGTHFNHNAWAKLGMGLGSHDYQIVNTEG 121

QY 179 YFSSGSASITVS 190  
DB 122 YOSSGSATITVS 133

RESULT 8  
US-09-909-207-3  
Sequence 3, Application US/09909207  
Patent No. US20020115181A1  
GENERAL INFORMATION:  
APPLICANT: ANDREE LAHAYE  
ERIC DE BUYL  
PIERRE LEDOUX  
RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,  
DNA molecule, processes for preparation of this xylanase  
and uses thereof  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE  
STREET: 2000 K St., N.W., Suite 200  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/909,207  
FILING DATE: 19-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: 08/470,953  
FILING DATE: 06-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilhlem F. Gadiano, Esq.  
REGISTRATION NUMBER: 37,136  
REFERENCE/DOCKET NUMBER: 4121-40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-0625  
TELEFAX: (202) 293-1850  
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 221 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-909-207-3

Query Match 45.0%; Score 470; DB 10; Length 221;  
Best Local Similarity 48.1%; Pred. No. 2.2e-34;  
Matches 91; Conservative 28; Mismatches 58; Indels 12; Gaps 3;

QY 8 GYNNGYFYSYWNDRHGGVYTYTNGPGQSFQSVNNSGNSGVYGGK-----WPGTKNK 58  
DB 9 GNHDGYDYEFWKDSGSGTMIILNHGCTFSAQNNVNNILFRGKKFNETQTHQOQVG--NM 66  
QY 59 VTFSGSYNPNGLSVYQWNRNPLIEYIVENFGYINPSTGATKLGVTSDGVSVDIY 118  
DB 67 SINYGANFQPNAGNAYLCVYGTWPLVEYIYVDSWGNWRP-PCATPKGTITVDGGTYDIY 125  
QY 119 RTORVNQPSIIG-TATFYQWVSRRNHRSSGVSNTANHNAAQOGLTLCMTDYOIIVAVEG 178  
DB 126 ETLRVNQPISIKGIATFKQIWSVRRSARTSGTISVSNHFRANLGNMGMKMEVALTVEG 185  
QY 179 YFSSGSASI 187  
DB 186 YOSSGSANV 194

RESULT 9  
US-09-909-207-6  
Sequence 6, Application US/09909207  
Patent No. US20020115181A1  
GENERAL INFORMATION:  
APPLICANT: ANDREE LAHAYE  
ERIC DE BUYL  
PIERRE LEDOUX  
RENE DETROZ  
TITLE OF INVENTION: Xylanase, microorganisms produced it,  
DNA molecule, processes for preparation of this xylanase  
and uses thereof  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE  
STREET: 2000 K St., N.W., Suite 200  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/909,207  
FILING DATE: 19-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: 08/470,953  
FILING DATE: 06-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilhlem F. Gadiano, Esq.  
REGISTRATION NUMBER: 37,136  
REFERENCE/DOCKET NUMBER: 4121-40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-0625  
TELEFAX: (202) 293-1850  
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-909-207-6

Query Match 45.0%; Score 470; DB 10; Length 248;  
Best Local Similarity 48.1%; Pred. No. 2.5e-34;  
Matches 91; Conservative 28; Mismatches 58; Indels 12; Gaps 3;

QY 8 GYNNGYFYSYWNDRHGGVYTYTNGPGQSFQSVNNSGNSGVYGGK-----WPGTKNK 58  
DB 36 GNHDGYDYEFWKDSGSGTMIILNHGCTFSAQNNVNNILFRGKKFNETQTHQOQVG--NM 93

Qy 59 VINFSGSNPNNGSYLSYVGRNPLIEYIVENFGTYNPSTGATKGEVTSDBGVYDIY 118  
 Db 94 SINGANFQPNAGNAYLCVYGTVDPLVYIYVDSWGNRP-PGATPKGTIIVDGGTYDIY 152  
 Qy 119 RTQRVQPSIIGTATFYQYWSVRNHRSSGVSNTANHNANAAQOGLTLGTMDYQIVAVEG 178  
 Db 153 ETLRVNPSIKGIATFKQYWSVRNHRSSGVSNTANHNANAAQOGLTLGTMDYQIVAVEG 212  
 Qy 179 YFSSGSASI 187  
 Db 213 YQSSGSANV 221

RESULT 10  
 US-09-970-616-2  
 : Sequence 2, Application US/09970616  
 : Patent No. US20020164399A1  
 : GENERAL INFORMATION:  
 : APPLICANT:  
 : SOUPPE, Jerome  
 : BEUDEKER, Robert Franciscus  
 : TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF ALCOHOLIC BEVERAGES USING MAIL

: NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LADAS & PARRY  
 : STREET: 26 WEST 61 STREET  
 : CITY: <Unknown>  
 : STATE: (E) ZIP CODE: 10023

: COUNTRY: USA  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: Microsoft Windows for Workgroups  
 : SOFTWARE: WordPerfect 8  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/970.616  
 : FILING DATE: 04-Oct-2001  
 : CLASSIFICATION: 435

: PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 09/230.590  
 : FILING DATE: 28-APR-1999  
 : APPLICATION NUMBER: PCT/EP97/04016  
 : FILING DATE: 23-JUL-1997  
 : APPLICATION NUMBER: EP 96202195.2  
 : FILING DATE: 05-AUG-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MASS, CLIFFORD J.  
 : REGISTRATION NUMBER:  
 : (C) REF./DOCKET NO.: U-012094-9

: TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 233288  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 185 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-970-616-2

Query Match 41.4%; Score 433; DB 9; Length 185;  
 Best Local Similarity 47.9%; Pred. No. 3.5e-31;  
 Matches 90; Conservative 25; Mismatches 63; Indels 10; Gaps 5;

Qy 6 GTGNNGYFYSYVNDGHHGGVYTNNGPGGQFSVNNNSN--SGNFGVKGWQPGTKNKNVNF 63  
 Db 4 GINIVQNY-----NGNLGDFYDES-AGTFSYHEDGVSSDFVGLGWTGSSN-AITYS 56  
 Qy 64 GSYNPNGN-SYLSYVGRNPLIEYIVENFGTYNPSTGATKGLGEVTSDBGVYDIYQTR 122

Db 57 AEYSASGSASYLAVYGVWVYQAEYIYVEDYGDYNPCSSATSLGTVYSDGTYQVQDTR 116  
 Qy 123 VNQPSIIGTATFYQYWSVRNHRSSGVSNTANHNANAAQOGLTLGTMDYQIVAVEGYFSS 182  
 Db 117 TNEFSIIGTSTFTQYFVSRESTRISGTYVANHNANAAQOGLTLGTMDYQIVAVEG 176  
 Qy 183 GSASITVS 190  
 Db 177 GSASVTVS 184

RESULT 11  
 US-09-790-070A-9  
 : Sequence 9, Application US/09790070A  
 : Publication No. US20030053999A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Jonniaux, Jean-Luc  
 : APPLICANT: Dauvin, Thierry  
 : TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY  
 : FILE REFERENCE: VANMI99.001AUS  
 : CURRENT APPLICATION NUMBER: US/09/790.070A  
 : CURRENT FILING DATE: 2001-02-21  
 : PRIOR APPLICATION NUMBER: EP 00870028.8  
 : PRIOR FILING DATE: 2000-02-21  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 9  
 : LENGTH: 84  
 : TYPE: PRT  
 : ORGANISM: Penicillium griseofulvum  
 US-09-790-070A-9

Query Match 16.9%; Score 177; DB 9; Length 84;  
 Best Local Similarity 58.3%; Pred. No. 7.6e-09;  
 Matches 28; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 8 GYNNGYFYSYVNDGHHGGVYTNNGPGGQFSVNNNSN--SGNFGVKGWQPGTKNKNVNF 55  
 Db 35 GTNGGYFYSYVNDGHHGGVYTNNGPGGQFSVNNNSN--SGNFGVKGWQPGTKNKNVNF 82

RESULT 12  
 US-09-996-634-131  
 : Sequence 131, Application US/09996634  
 : Patent No. US20020172684A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Nano, Francis  
 : TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding  
 : TITLE OF INVENTION: Immunostimulatory Peptides.  
 : FILE REFERENCE: 61260  
 : CURRENT APPLICATION NUMBER: US/09/996.634  
 : CURRENT FILING DATE: 2001-11-28  
 : PRIOR APPLICATION NUMBER: 09/447,135  
 : PRIOR FILING DATE: 2000-01-03  
 : PRIOR APPLICATION NUMBER: 08/990,823  
 : PRIOR FILING DATE: 1997-12-15  
 : PRIOR APPLICATION NUMBER: US 96/10375  
 : PRIOR FILING DATE: 1996-06-14  
 : PRIOR APPLICATION NUMBER: 60/000,254  
 : PRIOR FILING DATE: 1995-06-15  
 : NUMBER OF SEQ ID NOS: 169  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 131  
 : LENGTH: 943  
 : TYPE: PRT  
 : ORGANISM: Mycobacterium tuberculosis  
 US-09-996-634-131

Query Match 10.3%; Score 107.5; DB 9; Length 943;  
 Best Local Similarity 27.2%; Pred. No. 0.18; 79; Indels 51; Gaps 13;  
 Matches 58; Conservative 25; Mismatches 79; Indels 51; Gaps 13;

Qy 7 TGNNGYFYSYVNDGHHGGVYTNNGPGGQFSVNNNSN--NFGV---GKG-----WQPGTKN 57





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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:15:41 ; Search time 30 Seconds  
(without alignments)  
1304.965 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGGYFYSYWND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1045	100.0	223	3	Q02244 trichoderma
2	1033	98.9	223	3	Q99015 trichoderma
3	876	83.8	223	3	Q9UVF9 trichoderma
4	765.5	73.3	241	3	Q12580 chaetomium
5	705.5	67.5	219	3	Q12579 chaetomium
6	701.5	67.1	232	3	Q9HFA4 aspergillus
7	696.5	66.7	290	3	Q9HEZ0 phanerochaete
8	686.5	66.7	290	3	Q9HEY9 phanerochaete
9	686.5	65.7	295	3	Q9C1R2 fusarium ox
10	680.5	65.1	227	3	Q00263 ascochyta p
11	678.5	64.9	227	3	Q9UVZ3 helminthosp
12	665.5	63.7	225	3	Q9HTG2 aspergillus
13	656	62.8	221	3	Q9UQU2 penicillium
14	647.5	62.0	223	3	Q9HFR0 penicillium
15	635.5	60.8	231	3	Q13447 cochliobolu
16	632.5	60.5	346	2	Q8VUT4 pseudomonas

17	629.5	60.2	221	3	P87037
18	628.5	60.1	231	3	Q00350
19	623.5	59.7	194	3	P81536
20	615.5	58.9	227	3	Q9HGE1
21	613.5	58.7	283	3	Q96UV7
22	609.5	58.3	335	2	Q08346
23	609.5	58.3	335	2	Q9RMW4
24	608.5	58.2	335	2	Q9RQB8
25	607.5	58.1	338	2	Q56265
26	606.5	58.0	231	3	Q9C1R1
27	598	57.2	228	2	Q59962
28	596	57.0	216	3	Q74716
29	591.5	56.6	329	2	Q9RMH9
30	591	56.6	335	16	Q9RKN6
31	567	54.3	191	2	Q9EW89
32	536.5	51.3	661	2	Q59674
33	530.5	50.8	241	16	Q9RI72
34	528.5	50.6	361	2	Q52375
35	526.5	50.4	656	2	Q59300
36	525	50.2	240	2	Q56013
37	524.5	50.2	210	16	Q9KEF3
38	524.5	50.2	360	2	P77853
39	520	49.8	357	2	Q8VP72
40	515.5	49.3	211	2	Q43993
41	511	48.9	213	2	Q8VVC3
42	504.5	48.3	213	2	Q9ZB36
43	503	48.1	213	2	Q59254
44	502	48.0	213	2	Q59256
45	501	47.9	217	5	Q97402

#### ALIGNMENTS

#### RESULT 1

ID	Q02244	PRELIMINARY;	PRT;	223 AA.
AC	Q02244;			
DC	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DE	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
GN	Endoxylanase II.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; Hypocreaceae; Hypocrea.			
OX	NCBI_TaxID=51453;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94088442; PubMed=8264524;			
RA	Saarelainen R., Paloheimo M., Fagerstrom R., Suominen P.L.,			
RA	Nevalainen K.M.;			
RT	"Cloning, sequencing and enhanced expression of the Trichoderma reesei			
RT	endoxylanase II (pr 9) gene xln2.;"			
RL	Mol. Gen. Genet. 241:497-503(1993).			
DR	EMBL; S67387; AAB29346.1; -			
DR	HSSP; P36217; 1XYO.			
DR	InterPro; IPR001137; GH11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLYDRLASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_Fil_1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_Fil_2; 1.			
KW	Glycosidase; Hydrolase; Xylan degradation.			
SQ	SEQUENCE 223 AA; 24069 MW; 75668149EADA22F9 CRC64;			

Query Match 100.0%; Score 1045; DB 3; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.4e-68;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OTIQPGTGYNGGYFYSYWNDGGGVYTYTNGPGQFVSNVNSGNFVGKGQPGTKNKVI 60

Db 34 QTIQPGTGYNGGYFYSYWNDGGGVYTYTNGPGQFVSNVNSGNFVGKGQPGTKNKVI 93

```
QY 61 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 120
|||||
Db 94 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 153
|||||
QY 121 QRVNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
|||||
Db 154 QRVNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 213
|||||
QY 181 SSGSASITVS 190
|||||
Db 214 SSGSASITVS 223
|||||

RESULT 2
Q99015 PRELIMINARY; PRT; 223 AA.
AC Q99015;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Beta-xylanase precursor.
GN XYN2
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OM 6A;
RX MEDLINE=97076932; PubMed=8975597;
RA la Grange D.C., Pretorius I.S., van Zyl W.H.;
RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
RT Saccharomyces cerevisiae."
RL Appl. Environ. Microbiol. 62:1036-1044(1996).
DR EMBL; U24191; AAB50278.1;
DR HSSP; P36217; LXVO.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 223 BETA-XYLANASE.
FT SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;
Best Local Similarity 98.9%; Pred. No. 5.4e-67;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTOPGTGYNNGYFYSYWNDGCGVYTTNGPGQGFVSNNNSNGFVGGKWPQGTKNKVI 60
|||||
Db 34 QTOPGTGYNNGYFYSHYWNDGCGVYTTNGPGQGFVSNNNSNGFVGGKWPQGTKNKVI 93
|||||
QY 61 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 120
|||||
Db 94 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 153
|||||
QY 121 QRVNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
|||||
Db 94 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 153
|||||
QY 181 SSGSASITVS 190
|||||
Db 214 SSGSASITVS 223
|||||

RESULT 3
Q9UVF9 PRELIMINARY; PRT; 223 AA.
AC Q9UVF9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
```

```
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS Trichoderma viride.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5547;
RN [1]
RP SEQUENCE FROM N.A.
RA Furman-Matarasso N., Cohen E., Avni A.;
RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
RT Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the
RT Elicitation Activity."
RL Submitted (NOV-1998) to the EMBL/GenBank/DDJB databases.
DR EMBL; AJ012718; CAB60757.1;
DR HSSP; P48793; 1XND.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.
FT SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;
Best Local Similarity 82.1%; Pred. No. 1e-55;
Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QTOPGTGYNNGYFYSYWNDGCGVYTTNGPGQGFVSNNNSNGFVGGKWPQGTKNKVI 60
|||||
Db 34 QTOPGTGYNNGYFYSYWNDGCGVYTTNGAGGFSVNNANSNGFVGGKWPQGTKNKVI 93
|||||
QY 61 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 120
|||||
Db 94 NFGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSFGSVYDIYRT 153
|||||
QY 121 QRVNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
|||||
Db 154 QRVNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 213
|||||
QY 181 SSGSASITVS 190
|||||
Db 214 SSGSASITVS 223
|||||

RESULT 4
Q12580 PRELIMINARY; PRT; 241 AA.
AC Q12580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Endo-beta1,4-xylanase (EC 3.2.1.8).
GN CGXB.
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96118924; PubMed=8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans."
RL Curr. Genet. 29:73-80(1995).
DR EMBL; D49851; BAA08650.1;
DR HSSP; P36217; LXVO.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
FT SIGNAL 1 33 POTENTIAL.
FT SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;
```



Query Match 73.3%; Score 765.5; DB 3; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 9.8e-48;  
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

Qy 7 TGYNNGYYSYWNHGGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGSY 66  
 Db 38 TGTNNGYYSFTWTDGQGNVQTNAGGQYSVTWNGNWNVGGKGNPGSA-RTINYTANY 96

Qy 67 NPNGNSYLSVWGSNRNPLIEYIIVENFGTYNPSTGATKLGVTSDGSYDIYRTQVNOP 126  
 Db 97 NPNGNSYLSVWGSNRNPLIEYIIVENFGTYNPSTGATKLGVTSDGSYDIYRTQVNOP 156

Qy 127 SIIGTATFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 186  
 Db 157 SIEGTSTFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 216

Qy 187 ITV 189  
 Db 217 VNV 219

RESULT 5  
 Q12579 PRELIMINARY; PRT; 219 AA.

AC Q12579;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Endo-beta1,4-xylanase A (EC 3.2.1.8).  
 GN CGXA.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Chaetomiaceae; Chaetomium.  
 OX NCBI\_TaxID=47794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RT "Two family G xylanase genes from Chaetomium gracile and their  
 expression in Aspergillus nidulans".  
 RL Curr. Genet. 29:73-80(1995).  
 DR EMBL; D49850; BAA08649.1; -;  
 DR HSSP; P36217; 1XVO.  
 DR InterPro; IPR001137; GH\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_Fil\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_Fil\_2; 1.  
 KW Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9FBA CRC64;

Query Match 67.5%; Score 705.5; DB 3; Length 219;  
 Best Local Similarity 68.1%; Pred. No. 1.8e-43;  
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

Qy 6 GTGYNNGYYSYWNHGGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGS 65  
 Db 36 GTGTNNGYYSFTWTDGQGNVQTNAGGQYSVTWNGNWNVGGKGNPGSA-RTINFSGT 94

Qy 66 YNPNGNSYLSVWGSNRNPLIEYIIVENFGTYNPSTGATKLGVTSDGSYDIYRTQVNOP 125  
 Db 95 FSPQNGVLAIVGWTQNPVLEIYVESFTYDPSQSKFGTIOQDGSYIAKTRVNO 154

Qy 126 PSIIGTATFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 185  
 Db 155 PSIEGTSTFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 214

Qy 186 SITVS 190  
 Db 215 SITVS 219

RESULT 6  
Q9HFA4

Q9HFA4 PRELIMINARY; PRT; 232 AA.

AC Q9HFA4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Xylanase G2 (EC 3.2.1.8).  
 GN XNG2.  
 OS Aspergillus oryzae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=5062;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kimura T., Sakka K., Ohmiya K.;  
 RT "Molecular cloning, overexpression, and purification of major xylanase  
 from Aspergillus oryzae".  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB044941; BAB20794.1; -;  
 DR HSSP; P36217; 1XVO.  
 DR InterPro; IPR001137; GH\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_Fil\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_Fil\_2; 1.  
 KW Glycosidase; Hydrolase.  
 SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 67.1%; Score 701.5; DB 3; Length 232;  
 Best Local Similarity 67.8%; Pred. No. 3.7e-43;  
 Matches 124; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

Qy 7 TGYNNGYYSYWNHGGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGSY 66  
 Db 50 TGYNNGYYSYWNHGGVTTNGPGGQFSVNMNSGNFVGGKGNPGS-SRAITYSGSF 108

Qy 67 NPNGNSYLSVWGSNRNPLIEYIIVENFGTYNPSTGATKLGVTSDGSYDIYRTQVNOP 126  
 Db 109 NPNGNSYLSVWGSNRNPLIEYIIVENFGTYNPSTGATKLGVTSDGSYDIYRTQVNOP 168

Qy 127 SIIGTATFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 186  
 Db 169 SIIGTATFYQWSVRRNRHSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVGYSFSSGSAS 228

Qy 187 ITV 189  
 Db 229 ITV 231

RESULT 7  
 Q9HEZ0 PRELIMINARY; PRT; 290 AA.

AC Q9HEZ0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Endo-1,4-B-xylanase B.  
 GN XYNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OX NCBI\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;  
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
 RT "Molecular characterization and expression analysis of two endo-1,4-B-  
 xylanase genes from Phanerochaete chrysosporium".  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF301904; AAG44994.1; -;  
 DR HSSP; P00725; IAZ6.  
 DR InterPro; IPR000254; CBD\_fungal.

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DR InterPro: IPR001137; GH_11.
DR Pfam: PF00734; CBM_1; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR ProDom: PD001821; CBD_fungal; 1.
DR SMART: SM00236; fCBD; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 290 AA; 30425 MW; 6DIC6415370A667D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92

QY 61 NFGSGYNPNSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 120
DB 93 SFTANYQPNNGSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 152

QY 121 QRVNPSIICTATFYQYWSVRRNHRSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 153 TRVNEPSIOGTATFNQYWSIRSSKRSGVTVTANHFNAQAQGLTLGTMDYQIVAVEGYF 212

QY 181 SSGSASITVS 190
DB 213 SSGSSTVTVN 222

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92

QY 61 NFGSGYNPNSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 120
DB 93 SFTANYQPNNGSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 152

QY 121 QRVNPSIICTATFYQYWSVRRNHRSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 153 TRVNEPSIOGTATFNQYWSIRSSKRSGVTVTANHFNAQAQGLTLGTMDYQIVAVEGYF 212

QY 181 SSGSASITVS 190
DB 213 SSGSSTVTVN 222

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92
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DR InterPro: IPR001137; GH_11.
DR Pfam: PF00734; CBM_1; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR ProDom: PD001821; CBD_fungal; 1.
DR SMART: SM00236; fCBD; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 290 AA; 30425 MW; 6DIC6415370A667D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92

QY 61 NFGSGYNPNSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 120
DB 93 SFTANYQPNNGSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 152

QY 121 QRVNPSIICTATFYQYWSVRRNHRSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 153 TRVNEPSIOGTATFNQYWSIRSSKRSGVTVTANHFNAQAQGLTLGTMDYQIVAVEGYF 212

QY 181 SSGSASITVS 190
DB 213 SSGSSTVTVN 222

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92

QY 61 NFGSGYNPNSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 120
DB 93 SFTANYQPNNGSYLSVYGWSRNPLEYIYVENFGTYNPNSTGATKLGVEVTSYDGYDIYRT 152

QY 121 QRVNPSIICTATFYQYWSVRRNHRSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 153 TRVNEPSIOGTATFNQYWSIRSSKRSGVTVTANHFNAQAQGLTLGTMDYQIVAVEGYF 212

QY 181 SSGSASITVS 190
DB 213 SSGSSTVTVN 222

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 1.1e-42;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTTPGTYNGNGYFYSVWNGDGHGVTTNGPGGQFSVWNSNGFVGKGGWOPGTRKNKI 60
DB 34 QSTPAGTGTNGGYFSEFTWDGGSVYNNNGPAGEYSVTSNADNFVAGKGNPGSA-QAI 92
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OC mitosporic Pezizomycotina; Ascomycota.
OX NCBI_TaxID=47971;
RN [1]
RP SEQUENCE FROM N.A.
RA Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RL pathogenic fungus Ascochyta pisi Lib.,"
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z68891; CA93120.1; -
DR HSSP: O43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL-HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL-HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1
FT CHAIN 19
FT POTENTIAL 19
SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0P CRC64;

Query Match 65.1%; Score 680.5; DB 3; Length 227;
Best Local Similarity 65.3%; Pred. No. 1.2e-41;
Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;

Qy 2 TIQPGT----CYNNGFYFSYVNDGCHGGVYTNPGGQFSVNWNSGNFVGGKGNPGTKN 57
Db 34 TARAGTPSSQGTTHNGCFYSWMTDGGAAQATYTNAGAGSYSVNKKTGGLVGGKGNPGAA- 92
Qy 58 KVINFGSYNPGNSYLSVYGWSRNPPLIEYIVENFGTYNPSTGATKLGVEYTSFGSVYDI 117
Db 93 RTIYSGTYSFGNSYLAIVGWRNPPLIEYIVVENFGTYDPSSQATYKSGVTAGSSYKI 152
Qy 118 YRTQVNPQSIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDYQI 177
Db 153 AQOTRNPQSIDGTRTFQYQWSVRNRHRSRSGSVNKKTHFDAAWASKMNLGSHYQI 212
Qy 178 GFSSGASITVS 190
Db 213 GFSSGSAQITVN 225

RESULT 11
Q9UV23 ID Q9UV23 PRELIMINARY; PRT; 227 AA.
AC Q9UV23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Xylanase precursor.
GN XYL1.
OS Helminthosporium turcicum.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Helminthosporium.
OX NCBI_TaxID=93612;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=H2;
RC Degefu Y., Paulin L., Peraenen J., Lubeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RL pathogen Helminthosporium turcicum Pass.,"
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ238895; CAB52417.1; -
DR HSSP: O43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL-HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL-HYDROL_F11_2; 1.
KW Signal.
FT SIGNAL 1
FT CHAIN 20
FT POTENTIAL 19
FT XYLANASE 20
SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;

Query Match 64.9%; Score 678.5; DB 3; Length 227;
Best Local Similarity 64.7%; Pred. No. 1.6e-41;

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Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;
Qy 1 OTIQPGTGYNNGFYFSYVNDGCHGGVYTNPGGQFSVNWNSGNFVGGKGNPGTKNKVI 60
Db 37 QSTPNGEHTHNGCFYSWMDGGRATYTNAGAGSYSVSWGTGGNLVGGKGNPGTA-RTI 95
Qy 61 NFSGYNPNNGNSYLSVYGWSRNPPLIEYIVENFGTYNPSTGATKLGVEYTSFGSVYDI 120
Db 96 TYSQYNPNGNSYLAIVGWRNPPLIEYIVVENFGTYDPSSQAQNGTIVTSDESSYKIAQS 155
Qy 121 ORVNPQSIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDYQI 180
Db 156 TRTNQPSIDGTRTFQYQWSVRNRHRSRSGSVNKKTHFDAAWASKMNLGSHYQI 215
Qy 181 SSGSASITVS 190
Db 216 SSGSASITVN 225

RESULT 12
Q8TG22 ID Q8TG22 PRELIMINARY; PRT; 225 AA.
AC Q8TG22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endo-1,4-xylanase.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu S., Sun J., Xu Z., Li W., Zhao H.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF490982; AAM08362.1; -
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 225 AA; 24127 MW; 5B14121662842A10 CRC64;

Query Match 63.7%; Score 665.5; DB 3; Length 225;
Best Local Similarity 65.6%; Pred. No. 1.4e-40;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
Qy 7 TGYNNGFYFSYVNDGCHGGVYTNPGGQFSVNWNSGNFVGGKGNPGTKNKVNFSGSY 66
Db 43 TGENNGFYFSYVNDGCHGGVYTNPGGQFSVNWNSGNFVGGKGNPGSAQD-ITYSGTF 101
Qy 67 NPNGNSYLSVYGWSRNPPLIEYIVENFGTYNPSTGATKLGVEYTSFGSVYDIYRTQVNP 126
Db 102 TPGSGNYSYVYGWTDPLIEYIVESYDYNPGSGGTGTYKGTIVTSFGSVYDIYATRTNAA 161
Qy 127 SIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDYQI 186
Db 162 SIQGTATFYQYWSVRNRHRSRSGSVNTSNHFNWAKLGNLGNLGNLGNLGNLGNLGNLGN 221
Qy 187 ITV 189
Db 222 ITV 224

RESULT 13
Q9UUQ2 ID Q9UUQ2 PRELIMINARY; PRT; 221 AA.
AC Q9UUQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Xylanase A (EC 3.2.1.8).
GN XYNA.
OS Penicillium sp. 40.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=110511;

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GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:13:11 ; Search time 76 Seconds  
(without alignments)  
333.127 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTNGYNGYFSYWD.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	190	19	Xylanase II of Tri
2	1045	100.0	190	21	T. reesei xylanase
3	1045	100.0	190	23	Trichoderma reesei
4	1045	100.0	223	14	pi 9.0 endoxylanase
5	1045	100.0	223	20	T. reesei xylanase
6	1042	99.7	190	23	Trichoderma reesei
7	1040	99.5	190	21	Trichoderma reesei
8	1038	99.3	190	19	Modified xylanase
9	1038	99.3	190	23	Trichoderma reesei
10	1035	99.0	190	19	Xylanase of Tricho

11	1035	99.0	190	21	AAV99681	T. viride xylanase
12	1035	99.0	190	23	AAE18453	Trichoderma viride
13	1030	98.6	190	21	AAV99735	Mutant T. reesei x
14	1029	98.5	190	23	AAE18495	Trichoderma reesei
15	1024	98.0	190	23	AAE18496	Trichoderma reesei
16	1023	97.9	190	23	AAE18472	Trichoderma reesei
17	1022	97.8	190	21	AAE18476	Trichoderma viride
18	1020	97.6	190	23	AAE18476	Trichoderma reesei
19	1017	97.3	190	23	AAE18474	Trichoderma reesei
20	1017	97.3	190	23	AAE18475	Trichoderma reesei
21	1017	97.3	190	23	AAE18482	Trichoderma reesei
22	1016	97.2	190	23	AAE18473	Trichoderma reesei
23	1016	97.2	223	19	AAW57422	Amino acid sequenc
24	1014	97.0	190	23	AAE18478	Trichoderma reesei
25	1014	97.0	190	23	AAE18481	Trichoderma reesei
26	1013	96.9	190	23	AAE18477	Trichoderma reesei
27	1013	96.9	190	23	AAE18480	Trichoderma reesei
28	1012	96.8	190	23	AAE18479	Trichoderma reesei
29	1010	96.7	190	23	AAE18483	Trichoderma reesei
30	1001	95.8	190	23	AAE18487	Trichoderma reesei
31	1000	95.7	190	23	AAE18484	Trichoderma reesei
32	1000	95.7	190	23	AAE18485	Trichoderma reesei
33	999	95.6	190	23	AAE18486	Trichoderma reesei
34	996	95.3	190	19	AAW60741	Xylanase of Tricho
35	996	95.3	190	21	AAV99678	T. harzianum xylan
36	996	95.3	190	23	AAE18450	Trichoderma reesei
37	994	95.1	190	23	AAE18488	Trichoderma reesei
38	993	95.0	190	23	AAE18489	Trichoderma reesei
39	992	94.9	190	19	AAW60282	Modified xylanase
40	990	94.7	190	21	AAE18493	Trichoderma harzia
41	990	94.7	190	21	AAV99736	Mutant T. reesei x
42	986	94.4	190	23	AAE18490	Trichoderma reesei
43	978	93.6	190	23	AAE18491	Trichoderma reesei
44	969	92.7	190	23	AAE18493	Trichoderma reesei
45	962	92.1	190	23	AAE18494	Trichoderma reesei

#### ALIGNMENTS

RESULT 1

AAW60743

ID AAW60743 standard; protein; 190 AA.

XX AAW60743;

XX 02-SEP-1998 (first entry)

DT Xylanase II of Trichoderma reesei.

DE

XX

XX

KW

KW

KW

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OS

XX

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PN

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PD

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PF

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PR

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PA

PA

XX

PI

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DR

XX

PT

PT

XX Disclosure; Page 48; 84pp; English.  
 XX AAW60728-44 represent family 11 xylanases. The specification describes a  
 CC method for modifying a family 11 xylanase to improve its  
 CC thermophilicity, alkalophilicity and/or thermostability. This method  
 CC comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei  
 CC xylanase II or corresponding aligned amino acid sequences in the  
 CC xylanase, replacement of one or more amino acid sequences in the  
 CC N-terminal region with corresponding aligned sequences from another  
 CC family 11 xylanase to form a chimeric xylanase and/or upstream extension  
 CC of the N terminus by addition of up to 10 amino acids. The modified  
 CC xylanases are useful for improving the bleaching of wood pulp by  
 CC treatment at 53-75 degrees Celsius and pH 7.5-9.0 for 5-180 minutes. They  
 CC might also be useful as digestibility-improving animal feed additives.  
 CC They might also be useful in the processing of wheat or maize for starch  
 CC production.  
 XX Sequence 190 AA;  
 SQ

Query Match 100.0%; Score 1045; DB 19; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QTIQPGTGYNNGYFYSYWNDGCGVYTYNGPGQGFVSNNNSGNGFVGKQWPGTKNKVI 60  
 Db 1 QTIQPGTGYNNGYFYSYWNDGCGVYTYNGPGQGFVSNNNSGNGFVGKQWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSVLSVYGWSRNPGLIEYIVENFGTYNPSTGATKLGVEVSDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGNSVLSVYGWSRNPGLIEYIVENFGTYNPSTGATKLGVEVSDGSVYDIYRT 120  
 QY 121 QRYNQPSIICTATFYQVWSVRRNRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 Db 121 QRYNQPSIICTATFYQVWSVRRNRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 2  
 AAY99680  
 ID AAY99680 standard; protein; 190 AA.  
 AC AAY99680;  
 DT 28-SEP-2000 (first entry)  
 XX T. reesei xylanase, Xyn II.  
 DE Xylanase; animal feed; digestion efficiency; thermostable;  
 KW feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.  
 XX Trichoderma reesei.  
 OS  
 XX WO200029587-A1.  
 XX 25-MAY-2000.  
 XX 16-NOV-1999; 99WO-CA01093.  
 XX 16-NOV-1998; 98US-0108504.  
 XX (IOGE-) IOGEN CORP.  
 XX Sung WL, Tolan JS;  
 XX WPI; 2000-387799/33.  
 XX N-PSDB; AAA48219.  
 XX Thermostable xylanases useful for preparing animal feeds especially  
 PT poultry or swine feed, exhibits optimal activity under physiological

PT Conditions -  
 XX Disclosure; Fig 1; 86pp; English.  
 XX Xylanase enzymes are added to animal feeds to increase the efficiency of  
 CC digestion and assimilation of nutrients. Xylanases are preferentially  
 CC added during the feed pelleting process. To survive the pelleting  
 CC process and to have optimum activity in the animal, the xylanase needs to  
 CC have high thermostability, with optimum activity at physiological pH and  
 CC temperature. The present sequence, xylanase Xyn II, from Trichoderma  
 CC reesei, is a xylanase family 11 member. The xylanases of family  
 CC 11 have several properties suitable for feed applications, however, they  
 CC lack the thermostability required to survive food pelleting. The present  
 CC sequence was used to identify non-conserved residues in family 11  
 CC xylanases which could be mutated to introduce desirable properties e.g.  
 CC thermostability. As a result various thermostable xylanases were  
 CC identified (AAY99683, AAY99684, AAY99685, AAY99686, AAY99735 and  
 CC AAY99736) which would be useful for animal feeds, especially poultry and  
 CC swine feed.  
 XX Sequence 190 AA;  
 SQ

Query Match 100.0%; Score 1045; DB 21; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QTIQPGTGYNNGYFYSYWNDGCGVYTYNGPGQGFVSNNNSGNGFVGKQWPGTKNKVI 60  
 Db 1 QTIQPGTGYNNGYFYSYWNDGCGVYTYNGPGQGFVSNNNSGNGFVGKQWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSVLSVYGWSRNPGLIEYIVENFGTYNPSTGATKLGVEVSDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGNSVLSVYGWSRNPGLIEYIVENFGTYNPSTGATKLGVEVSDGSVYDIYRT 120  
 QY 121 QRYNQPSIICTATFYQVWSVRRNRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 Db 121 QRYNQPSIICTATFYQVWSVRRNRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 3  
 AAE18452  
 ID AAE18452 standard; Protein; 190 AA.  
 XX AAE18452;  
 AC AAE18452;  
 DT 16-MAY-2002 (first entry)  
 XX Trichoderma reesei xylanase (TRX), Xyn II.  
 DE Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II.  
 XX Trichoderma reesei.  
 OS  
 XX Key Location/Qualifiers  
 FT Region 151..162  
 FT /note="Helix"  
 XX WO200192487-A2.  
 XX 06-DEC-2001.  
 XX 31-MAY-2001; 2001WO-CA00769.  
 XX 31-MAY-2000; 2000US-213803P.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 PI

XX WPI; 2002-171435/22.  
 DR N-PSDB; AAD29410.  
 XX  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing  
 XX  
 XX  
 PS Disclosure: Page 80-81; 109pp; English.  
 XX  
 CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is  
 CC Trichoderma reesei xylanase (trX), Xyn II.  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 1045; DB 23; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QTIQPGTGYNNGYFYSYWNDSYVNDGSGVYTNPGGQFVSVMNSGNSGFGKQWPGTKNKVI 60  
 Db 1 QTIQPGTGYNNGYFYSYWNDSYVNDGSGVYTNPGGQFVSVMNSGNSGFGKQWPGTKNKVI 60  
 Qy 61 NFSGSYNPNNGNSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGNSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHRSVNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 180  
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHRSVNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 180  
 Qy 131 SSGSASITVS 190  
 Db 181 SSGSASITVS 190  
 RESULT 4  
 AAR47122  
 ID AAR47122 standard; Protein; 223 AA.  
 XX  
 AC AAR47122;  
 XX 10-JUN-1994 (first entry)  
 XX  
 XX pI 9.0 endoxylanase.  
 DE Trichoderma reesei; enzyme; paper; pulp; food; feed industry;  
 KW pI 5.5; pI 9.0; xln1; xln2; endoxylanase.  
 XX Trichoderma reesei QM6a.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 34..223  
 FT /label= mat\_protein  
 FT Peptide 83..89  
 FT /note= "sequence used for prepn. of PCR primer"  
 FT Cleavage-site 19..20  
 FT Modified-site 71  
 FT /label= N-glycosylation\_site  
 FT Modified-site 94  
 FT /label= N-glycosylation\_site  
 FT Active-site 119  
 FT /note= "Glu proposed to be involved with an  
 FT active site"  
 FT Active-site 210  
 FT /note= "Glu proposed to be involved with an

FT XX WO9324621-A. active site\*  
 PN XX  
 XX  
 PD 09-DEC-1993.  
 XX  
 PF 24-MAY-1993; 93WO-FI00221.  
 XX  
 XX 29-MAY-1992; 92US-0889893.  
 XX  
 XX (ALKO-) ALKO OY AB.  
 XX  
 XX Pagarstrom R, Lahtinen T, Nevalainen H, Paloheimo M;  
 PI Saarelainen, Suominen P;  
 PI  
 DR WPI; 1993-405812/50.  
 DR N-PSDB; AAQ54775.  
 XX  
 XX Isolated nucleic acid mol. used in enzymes for paper, pulp and  
 PT feed industry - comprising sequence encoding aminoacid sequence  
 PT of T. reesei pI 5.5 xylanase  
 XX  
 XX Claim 3; Page 77-78; 111pp; English.  
 PS  
 XX The T. reesei xln2 gene coding for the pI 9.0 endoxylanase was  
 CC isolated from the wild-type strain QM6a. The gene contains one  
 CC intron of 108 nucleotides and codes for a protein of 223 amino  
 CC acids in which two putative N-glycosylation target sites were  
 CC found. Three different T. reesei strains were transformed by  
 CC targeting a construct composed of the xln2 gene with its own  
 CC promoter to the endogenous cbh1 locus. Highest overall prodn.  
 CC levels for xylanase were obtained using the T. reesei A.K02721,  
 CC a genetically engineered strain, as a host. Integration into  
 CC the cbh1 locus was not required for enhanced expression under  
 CC xln2 promoter.  
 XX  
 SQ Sequence 223 AA;  
 Query Match 100.0%; Score 1045; DB 14; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QTIQPGTGYNNGYFYSYWNDSYVNDGSGVYTNPGGQFVSVMNSGNSGFGKQWPGTKNKVI 60  
 Db 34 QTIQPGTGYNNGYFYSYWNDSYVNDGSGVYTNPGGQFVSVMNSGNSGFGKQWPGTKNKVI 93  
 Qy 61 NFSGSYNPNNGNSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 Db 94 NFSGSYNPNNGNSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 153  
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHRSVNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 180  
 Db 154 QRVNQPSTIGTATFYQYWSVRNRHRSVNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 213  
 Qy 181 SSGSASITVS 190  
 Db 214 SSGSASITVS 223  
 RESULT 5  
 AAW67567  
 ID AAW67567 standard; Protein; 223 AA.  
 XX  
 AC AAW67567;  
 XX  
 XX 02-MAR-1999 (first entry)  
 DT  
 XX  
 XX T. reesei xylanase II protein.  
 XX  
 XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;  
 KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.  
 XX  
 XX Trichoderma reesei.

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XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /note= "primary signal peptide"
FT Peptide 20..33
FT Protein /note= "propeptide"
FT FT 33..223
FT Modified-site /note= "mature xylanase II protein"
FT FT 71
FT Modified-site /note= "N-glycosylated"
FT FT 94
FT Modified-site /note= "N-glycosylated"
FT FT 119
FT Active-site /note= "active site residue"
FT FT 210
FT Active-site /note= "active site residue"
XX US5837515-A.
XX 17-NOV-1998.
XX 16-SEP-1993; 93US-0121436.
XX 16-SEP-1993; 93US-0121436.
XX 16-MAY-1990; 90US-0524308.
XX 29-MAY-1992; 92US-0889893.
XX 24-MAY-1993; 93WO-FI00221.
XX 18-JUN-1993; 93US-0078478.
XX (ALKO-) ALKO-YHTOET OY.
XX Fagerstroem R, Nevalainen H, Paloheimo M, Saarelainen R;
XX Suominen P;
XX WPI: 1999-023453/02.
XX N-PSDB; AAV81332.
XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
XX recombinant production of the enzyme, for use in paper and pulp
XX production
XX Claim 3; Fig 3A-B; 52pp; English.
XX This sequence represents the Trichoderma reesei xylanase II enzyme
XX (xln2) which has an isoelectric point (pI) of 9. The coding sequence
XX was isolated by reverse transcription PCR using the primers
XX AAV81333-V81335 based on amino acid sequence derived from the N-terminal
XX of the purified protein. The encoded protein contains a 33 amino acid
XX propeptide sequence with a primary signal peptide cleavage site between
XX residues 19-20. The mature protein comprises 190 amino acids with a
XX calculated molecular weight of 20.8 kD. The enzymes are used in the
XX degradation of the polymer xylan, one of the most abundant carbohydrate
XX components in plants. This is especially useful in the paper and pulp
XX making industry.
XX Sequence 223 AA;
Query Match 100.0%; Score 1045; DB 20; Length 223;
Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QTIQPTGYNNGYFYSYNDGHHGVYTYTNGPGQGSVNMNSGNTFVGGKGWPGTKNKVI 60
DB 1 QTIQPTGYNNGYFYSYNDGHHGVYTYTNGPGQGSVNMNSGNTFVGGKGWPGTKNKVI 93
QY 61 NFSGSYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 94 NFSGSYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 153
QY 121 QRNVQPSIIIGTATFYQYWSVRNRHSSGSSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180
DB 154 QRNVQPSIIIGTATFYQYWSVRNRHSSGSSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223
RESULT 6
AAE18470
ID AAE18470 standard; Protein; 190 AA.
AC AAE18470;
XX 16-MAY-2002 (first entry)
XX Trichoderma reesei xylanase mutant, TrX-75A.
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; muten.
XX Trichoderma reesei.
OS Synthetic.
XX Key Location/Qualifiers
XX FT Misc-difference 75 /note= "Wild type Ser substituted with Ala"
XX PN WO200192487-A2.
XX PD 06-DEC-2001.
XX 31-MAY-2001; 2001WO-CA00769.
XX 31-MAY-2000; 2000US-213803P.
XX (CANA ) NAT RES COUNCIL CANADA.
XX Sung WL;
XX WPI: 2002-171435/22.
XX Modified xylanase exhibiting increased thermostability and
XX alkalophilicity useful for industrial processing e.g. for pulp
XX manufacturing
XX Claim 42; Page -: 109pp; English.
XX The present invention relates to a modified xylanase exhibiting increased
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX useful for bleaching of pulp, processing of precision devices and
XX improving digestibility of poultry and swine feed. Modified xylanase has
XX improved performance at conditions of high temperature and pH and
XX exhibits improved thermostability and/or alkalophilicity in comparison to
XX corresponding native xylanase. The present sequence is Trichoderma reesei
XX xylanase (TrX) mutant.
XX Note: The present sequence is not shown in the specification but is
XX derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and
XX shown in page 80-81 of the specification.
XX Sequence 190 AA;
Query Match 99.7%; Score 1042; DB 23; Length 190;
Best Local Similarity 99.5%; Pred. No. 1.6e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QTIQPTGYNNGYFYSYNDGHHGVYTYTNGPGQGSVNMNSGNTFVGGKGWPGTKNKVI 60
DB 1 QTIQPTGYNNGYFYSYNDGHHGVYTYTNGPGQGSVNMNSGNTFVGGKGWPGTKNKVI 60
QY 61 NFSGSYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 QRNVQPSIIIGTATFYQYWSVRNRHSSGSSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180

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Db 121 QRYNPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 7  
AAB48541  
ID AAB48541 standard; Protein; 190 AA.

XX AAB48541;  
DT 05-MAR-2001 (first entry)  
XX Trichoderma reesei xyn II xylanase.  
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;  
KW bleaching agent.  
OS Trichoderma reesei.  
XX WO200068396-A2.  
PN 16-NOV-2000.  
XX 12-MAY-2000; 2000WO-US13172.  
XX 12-MAY-1999; 99US-0133714.  
XX (XENC-) XENCOR INC.  
XX Bentzien JM;  
PI WPI; 2000-679800/66.  
DR Non naturally occurring XA protein with enhanced thermophilicity,  
PT alkalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp -  
XX Disclosure; Fig 16J; 114pp; English.

CC The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermophilicity, alkalophilicity or thermostability relative  
CC to the naturally occurring B. circulans xylanase. They may be used as  
CC the active compound in a bleaching agent which is used for bleaching  
CC pulp.  
XX Sequence 190 AA;

Query Match 99.5%; Score 1040; DB 21; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.4e-89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TIQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVIN 61  
Db 2 TIQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVIN 61

QY 62 FSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFCTYNPSTCATKLGVTSDGSVYDIYRTQ 121  
Db 62 FSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFCTYNPSTCATKLGVTSDGSVYDIYRTQ 121

QY 122 RVNQPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYFS 181  
Db 122 RVNQPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYFS 181

QY 182 SSGSASITVS 190  
Db 182 SSGSASITVS 190

RESULT 8  
AAW60284

ID AAW60284 standard; protein; 190 AA.

XX AAW60284;  
DT 02-SEP-1998 (first entry)  
XX Modified xylanase II of Trichoderma reesei.

XX Family 11 xylanase; improve; thermophilicity; alkalophilicity;  
KW thermotolerance; bleach; wood pulp; processing; wheat; maize;  
KW digestibility-improving animal feed additive; starch production; mutant.

XX Synthetic.  
OS Trichoderma reesei.

XX Key Location/Qualifiers  
FH Misc-difference 14  
FT /label= Fl4X  
FT /note= "this residue can be Tyr or Phe"

XX EP828002-A2.

XX 11-MAR-1998.

XX 05-SEP-1997; 97EP-0115412.

XX 09-SEP-1996; 96US-0709912.

XX (CANA ) NAT RES COUNCIL CANADA.

XX (NARE-) NAT RES COUNCIL.

XX Ishikawa K, Sung WL, Yaguchi M;

XX WPI; 1998-161100/15.

XX Modified xylanase enzymes - useful for improving wood pulp  
PT bleaching, etc.

PS Claim 5; Page -; 84pp; English.

XX The present sequence represents a modified xylanase of Trichoderma  
CC reesei. The specification describes a method for modifying  
CC a Family 11 xylanase to improve its thermophilicity, alkalophilicity  
CC and/or thermostolerance. This method comprises modification of amino acids  
CC 10, 14, 27 or 29 of Trichoderma reesei xylanase II or the corresponding  
CC aligned amino acids of another Family 11 xylanase, replacement of one or  
CC more amino acid sequences in the N-terminal region with corresponding  
CC aligned sequences from another Family 11 xylanase to form a chimeric  
CC xylanase and/or upstream extension of the N terminus by addition of upto  
CC 10 amino acids. The modified xylanases are useful for improving the  
CC bleachability of wood pulp by treatment at 55-75 degrees celsius and  
CC pH 7.5-9.0 for 5-180 minutes. They might also be useful as  
CC digestibility-improving animal feed additives. They might also be useful  
CC in the processing of wheat or maize for starch production.  
CC note: this sequence does not appear in the specification; it was created  
CC using information provided.

XX Sequence 190 AA;

Query Match 99.3%; Score 1038; DB 19; Length 190;  
Best Local Similarity 99.5%; Pred. No. 3.8e-89;  
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVI 60

Db 1 QTQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFCTYNPSTCATKLGVTSDGSVYDIYRT 120  
|||||

Db 61 NFSGYNPNNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGCVTS DGSVVDIYRT 120  
 QY 121 QRVNQPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
 Db 121 QRVNQPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 9  
 AAEL18471  
 ID AAEL18471 standard; Protein; 190 AA.  
 AC AAEL18471;  
 DT 16-MAY-2002 (first entry)  
 DE Trichoderma reesei xylanase mutant, TrX-105H.  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutcin.  
 OS Trichoderma reesei.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 105  
 FT /note= "Wild type Leu substituted with His"  
 PN WO200192487-A2.  
 PD 06-DEC-2001.  
 PF 31-MAY-2001; 2001WO-CA00769.  
 PR 31-MAY-2000; 2000US-213803P.  
 XX (CANADA) NAT RES COUNCIL CANADA.  
 PI Sung WL;  
 DR WPI; 2002-171435/22.  
 PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing  
 XX Disclosure; Page -: 109pp; English.  
 CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (TrX) mutant.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from wild type xylanase referred as SEQ ID NO: 16 (AAEL18452) and  
 CC shown in page 80-81 of the specification.  
 XX Sequence 190 AA;  
 SQ

Query Match 99.3%; Score 1038; DB 23; Length 190;  
 Best Local Similarity 99.5%; Pred. No. 3.8e-89;  
 Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QTIQPTGYNNGYFYSYWNDHGHTYTNPGQGFVSNNNSGNSFVGGKGPOTKKNVI 60  
 Db 1 QTIQPTGYNNGYFYSYWNDHGHTYTNPGQGFVSNNNSGNSFVGGKGPOTKKNVI 60

QY 61 NFSGYNPNNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGCVTS DGSVVDIYRT 120  
 Db 61 NFSGYNPNNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGCVTS DGSVVDIYRT 120  
 QY 121 QRVNQPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
 Db 121 QRVNQPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 10  
 AA60744  
 ID AA60744 standard; protein; 190 AA.  
 AC AA60744;  
 DT 02-SEP-1998 (first entry)  
 DE Xylanase of Trichoderma viride.  
 KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;  
 KW thermotolerance; bleach; wood pulp; processing; wheat; maize;  
 KW digestibility-improving animal feed additive; starch production; mutant.  
 OS Trichoderma viride.  
 PN EP828002-A2.  
 PD 11-MAR-1998.  
 PF 05-SEP-1997; 97EP-0115412.  
 PR 09-SEP-1996; 96US-0709912.  
 XX (CANADA) NAT RES COUNCIL CANADA.  
 XX (NARE-) NAT RES COUNCIL.  
 PI Ishikawa K, Sung WL, Yaguchi M;  
 DR WPI; 1998-161100/15.  
 PT Modified xylanase enzymes - useful for improving wood pulp  
 PT bleaching, etc.  
 PS Disclosure; Pages 49-50; 84pp; English.  
 CC AA60728-44 represent family 11 xylanases. The specification describes a  
 CC method for modifying a family 11 xylanase to improve its  
 CC thermophilicity, alkalophilicity and/or thermostolerance. This method  
 CC comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei  
 CC xylanase II or corresponding aligned amino acids of another family 11  
 CC xylanase, replacement of one or more amino acid sequences in the  
 CC N-terminal region with corresponding aligned sequences from another  
 CC family 11 xylanase to form a chimeric xylanase and/or upstream extension  
 CC of the N terminus by addition of up to 10 amino acids. The modified  
 CC xylanases are useful for improving the bleaching of wood pulp by  
 CC treatment at 55-75 degrees Celsius and pH 7.5-9.0 for 5-180 minutes. They  
 CC might also be useful as digestibility-improving animal feed additives.  
 CC They might also be useful in the processing of wheat or maize for starch  
 CC production.  
 XX Sequence 190 AA;  
 SQ

Query Match 99.0%; Score 1035; DB 19; Length 190;  
 Best Local Similarity 98.9%; Pred. No. 7.2e-89;  
 Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QTIQPTGYNNGYFYSYWNDHGHTYTNPGQGFVSNNNSGNSFVGGKGPOTKKNVI 60  
 Db 1 QTIQPTGYNNGYFYSYWNDHGHTYTNPGQGFVSNNNSGNSFVGGKGPOTKKNVI 60

Db	1	QTQTGTGFNNGYFYSWNDGHGGVYTYTNGPGGQFVSNVNSNSNFGVGGKGWPGTKNKVI	60
Qy	61	NFSGSYNPNGNSYLSVYGWSRNPLIEYIVYENFGTYNPSTGATKLGCVTSDGSVYDIYRT	120
Db	61	NFSGSYNPNGNSYLSVYGWSRNPLIEYIVYENFGTYNPSTGATKLGCVTSDGSVYDIYRT	120
Qy	121	QRVNSIIIGTATFYQWSVRRNHRSSGSYNTANHFNAWAQQGLTLGTMDYQIVAVEGYF	180
Db	121	QRVNSIIIGTATFYQWSVRRNHRSSGSYNTANHFNAWAQQGLTLGTMDYQIVAVEGYF	180
Qy	181	SSGSASITVS	190
Db	181	SSGSASITVS	190

RESULT 11  
AAY99681  
ID AAY99681 standard; protein; 190 AA.

Xylanase enzymes are added to animal feeds to increase the efficiency of digestion and assimilation of nutrients. Xylanases are preferentially added during the feed pelleting process. To survive the pelleting process and to have optimum activity in the animal, the xylanase needs to have high thermostability, with optimum activity at physiological pH and temperature. The present sequence, xylanase xyn, from *Trichoderma viride*, is a xylanase family 11 member. The xylanases of Family 11 have several properties suitable for feed applications, however, they lack the thermostability required to survive food pelleting. The present sequence was used to identify non-conserved residues in Family 11 xylanases which could be mutated to introduce desirable properties e.g. thermostability. As a result various thermostable xylanases were identified (AA999683, AA999684, AA999685, AA999686, AA999735 and AA999736) which would be useful for animal feeds, especially poultry and swine feed.

Query Match 99.0%; Score 1035; DB 21; Length 190;  
Best Local Similarity 98.9%; Pred. No. 7.2e-99;  
Matches 188; Conservative 1; Mismatches 1; Indels 0; Caps 0;  
QY 1 QTPGTGYNGVIFYSWNDGHHGVVTYNGGGGFSYVNSGNGFVGGKGWPGTKNKVI 60

RESULT 12  
AAE18453  
ID AAE1

xx The present invention relates to a modified xylanase exhibiting increased  
CC thermostability and alkalophilicity. Modified xylanase is useful in  
CC industrial process such as pulp manufacturing. Modified xylanase is also  
CC useful for bleaching of pulp, processing of precision devices and  
CC improving digestibility of poultry and swine feed. Modified xylanase has  
CC improved performance at conditions of high temperature and pH and  
CC exhibits improved thermostability and/or alkalophilicity in comparison to  
CC corresponding native xylanase. The present sequence is  
CC *Trichoderma viride* xylanase, Xyn.  
CC

	Query Match	99.0%	Score 1035;	DB 23;	Length 190;
	Best Local Similarity	98.9%	Pred. No. 7.2e-89;		
	Matches 188;	Conservative	1;	Mismatches	0;
				Indels	Gaps
Qy	1	QTIIQPGTCYNNGYEYSYWNDCGHHGGVYTYNGPGGQFSVNNSGNFVGGKQWPGCTKNKVI	60		
Db	1	QTIIQPGTCGNNGYEYSYWNDCGHHGGVYTYNGPGGQFSVNNSGNFVGGKQWPGCTKNKVI	60		
Qy	61	NFGSGYNPNGNSYLSVYGSWNPLIEYYIVNFQTYNPGTATKILGEVTSDBGVVDIYRT	120		

Db	1	QTIQGTGFNNGYFYSYWMDHGGVTVYNTNGPGGQFVSNVNSNGFVGGKGWQGTGNKVI	60
Qy	61	NFSGSYNPNGNSYLSVYGWSRNPLIEYIIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT	120
Db	61	NFSGSYNPNGNSYLSVYGWSRNPLIEYIIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT	120
Qy	121	QRVNQPSIICTATFYQWYSVRRNRHSSGVSNTAHFNMAQOGLTGTMDYQIVAVEGYF	180
Db	121	QRVNQPSIICTATFYQWYSVRRNRHSSGVSNTAHFNMAQOGLTGTMDYQIVAVEGYF	180
Qy	181	SSGSASITVS 190	
Db	181	SSGSASITVS 190	
RESULT 14			
AAE18495			
ID	AAE18495 standard; Protein; 190 AA.		
XX	XX		
XX	AAE18495;		
XX	XX		
DT	16-MAY-2002 (first entry)		
XX	XX		
DE	Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.		
XX	XX		
KW	Modified xylanase; thermostability; alkalophilicity; Industrial process;		
KW	pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.		
XX	XX		
OS	Trichoderma reesei.		
OS	Synthetic.		
XX	XX		
FH	Key Location/Qualifiers		
FT	Misc-difference 161		
FT	/note= "Wild type Gln substituted with Arg"		
FT	Misc-difference 162		
FT	/note= "Wild type Gln substituted with His"		
FT	Misc-difference 165		
FT	/note= "Wild type Thr substituted with His"		
XX	XX		
PN	W0200192487-A2.		
XX	XX		
PD	06-DEC-2001.		
XX	XX		
PF	31-MAY-2001; 2001WO-CA00769.		
XX	XX		
PR	31-MAY-2000; 2000US-213803P.		
XX	XX		
PA	(CANADA ) NAT RES COUNCIL CANADA.		
XX	XX		
PI	Sung WL;		
PI	XX		
DR	WPI; 2002-171435/22.		
XX	XX		
PT	Modified xylanase exhibiting increased thermostability and		
PT	alkalophilicity useful for industrial processing e.g. for pulp		
PT	manufacturing		
XX	XX		
PS	Claim 42; Page -; 109pp; English.		
XX	XX		
CC	The present invention relates to a modified xylanase exhibiting increased		
CC	thermostability and alkalophilicity. Modified xylanase is useful in		
CC	industrial process such as pulp manufacturing. Modified xylanase is also		
CC	useful for bleaching of pulp, processing of precision devices and		
CC	improving digestibility of poultry and swine feed. Modified xylanase has		
CC	improved performance at conditions of high temperature and pH and		
CC	exhibits improved thermophilicity and/or alkalophilicity in comparison to		
CC	corresponding native xylanase. The present sequence is Trichoderma reesei		
CC	xylanase (Trx) mutant.		
CC	Note: The present sequence is not shown in the specification but is		
CC	derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and		
CC	shown in page 80-81 of the specification.		
XX	XX		
SQ	Sequence 190 AA;		
SQ	SQ		

CC improved performance at conditions of high temperature, and pH and  
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (TrX) mutant.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and  
 CC shown in page 80-81 of the specification.  
 XX  
 SQ Sequence 190 AA;

Query Match 98.0%; Score 1024; DB 23; Length 190;  
 Best Local Similarity 97.9%; Pred. No. 7.6e-88;  
 Matches 186; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNSGVNFGVGGKQWPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNSGVNFGVGGKQWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

Search completed: May 9, 2003, 10:19:29  
 Job time : 77 secs

Query Match 98.5%; Score 1029; DB 23; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 2.6e-88;  
 Matches 187; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNSGVNFGVGGKQWPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNSGVNFGVGGKQWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGMTDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 15  
 AAE18496  
 ID AAE18496 standard; Protein; 190 AA.  
 AC AAE18496;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Trichoderma reesei xylanase mutant, Trx-157D-161R-162H-165H.  
 XX  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.  
 XX  
 OS Trichoderma reesei.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 157  
 FT /note= "Wild type Asn substituted with Asp"  
 FT Misc-difference 161  
 FT /note= "Wild type Gln substituted with Arg"  
 FT Misc-difference 162  
 FT /note= "Wild type Gln substituted with His"  
 FT Misc-difference 165  
 FT /note= "Wild type Thr substituted with His"  
 XX  
 PN WO200192487-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 31-MAY-2001; 2001WO-CA00769.  
 XX  
 PR 31-MAY-2000; 2000US-213803P.  
 XX  
 PA (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 PI Sung WL;  
 XX  
 WI WPI; 2002-171435/22.  
 DR  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing -  
 XX  
 PS Claim 42; Page -, 109pp; English.  
 XX  
 CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has

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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:14:01 ; Search time 24 Seconds  
(without alignments)  
328.354 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTPQGTGYNNGYFYSYND.....YQIVAVEGYFSSGSATVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	1045	100.0	222	1 XYN2_TRIRE	P36217 trichoderma
2	990	94.7	190	1 XYN_TRIHA	P48793 trichoderma
3	684.5	65.5	225	1 XYN1_EMENI	P55332 emeritella
4	676.5	64.7	225	1 XYNB_ASPAK	P48824 aspergillus
5	670.5	64.2	221	1 XYN2_EMENI	P55333 emeritella
6	664.5	63.6	225	1 XYN2_ASPNG	P55330 aspergillus
7	650.5	62.2	221	1 XYN1_COCCA	Q06562 cochliobolus
8	635.5	60.8	225	1 XYN1_THELA	O43097 thermomyces
9	614.5	58.8	227	1 XYN1_HUMIN	P55334 humicola in
10	594	56.8	335	1 XYNB_STRLI	P26515 streptomyces
11	575.5	55.1	644	1 XYNB_CELFI	P54865 cellulomona
12	571.5	54.7	233	1 XYN2_MAGGR	P55335 magnaporthe
13	565.5	54.1	197	1 XYN1_SCHCO	P35809 schizophyll
14	527	50.4	240	1 XYN1_STRLI	P26220 streptomyces
15	525.5	50.3	210	1 XYN1_BACST	P45705 bacillus st
16	503	48.1	213	1 XYN1_BACSU	P48429 bacillus su
17	502	48.0	213	1 XYN1_BACCI	P09850 bacillus ci
18	461	44.1	228	1 XYN1_BACPU	P00694 bacillus pu
19	453.5	43.4	261	1 XYN1_CLOSA	P17137 clostridium
20	444	42.5	512	1 XYN1_CLOTR	P33558 clostridium
21	442.5	42.3	229	1 XYN1_TRIRE	P36218 trichoderma
22	430	41.1	211	1 XYN1_ASPNG	P55328 aspergillus
23	430	41.1	211	1 XYN1_ASPNG	P55329 aspergillus
24	428	41.0	211	1 XYN1_ASPTU	P55331 aspergillus
25	425	40.7	211	1 XYN3_ASPAK	P33557 aspergillus
26	402	38.5	954	1 XYN1_RUMFL	P29126 ruminococcu
27	383.5	36.7	802	1 XYN1_RUMFL	Q53317 ruminococcu
28	305	29.2	607	1 XYN1_NEOPA	P29127 neocalitmas
29	286.5	27.4	608	1 XYN1_FIBSU	P35811 fibrobacter
30	246	23.5	625	1 XYN1_FIRSP	Q12667 phycomyces s
31	98.5	9.4	159	1 GRPA_MEDFA	Q09134 medicago fa
32	98	9.4	414	1 PHAL_PSELE	P2090 pseudomonas
33	95	9.1	1829	1 FRPC_NEIMB	Q09195 neisseria m

34	93	8.9	793	1 D153_HAEIN	O22629 haemophilus
35	91.5	8.8	358	1 R022_XENLA	P51990 xenopus lae
36	91.5	8.8	2185	1 POLG_SVDVH	P16604 s genome po
37	91	8.7	513	1 GUX1_TRIVI	P19355 trichoderma
38	91	8.7	734	1 PSAB_WHEAT	P58386 triticum ae
39	91	8.7	735	1 PSAB_MAIZE	P04967 zea mays (m
40	90	8.6	734	1 PSAB_PINTH	P41640 pinus thunb
41	89.5	8.6	666	1 MUR2_ENTHR	P39046 enterococcu
42	89.5	8.6	678	1 YF48_MYCTU	Q10778 mycobacteri
43	89.5	8.6	1115	1 FRPA_NEIMC	P55126 neisseria m
44	89.5	8.6	1829	1 FRPC_NEIMC	P55127 neisseria m
45	89.5	8.6	2185	1 POLG_SVDVU	P13900 s genome po

## ALIGNMENTS

RESULT 1

1	XYN2_TRIRE	STANDARD:	PRT;	222 AA.
AC	P36217:			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)			
DE	(1,4-beta-D-xylan xylanohydrolase 2).			
GN	XYN2.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; Hypocreaceae; Hypocrea.			
OX	NCBI_TaxID=51453;			
RN	[1]			
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	STRAIN=C30;			
RX	MEDLINE=93103679; PubMed=1369024;			
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,			
RA	Harkki A., Kubicek C.P.;			
RT	"The two major xylanases from Trichoderma reesei: characterization of			
RT	both enzymes and genes."			
RL	Biotechnology 10:1461-1465(1992).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			
RC	STRAIN=C30;			
RX	MEDLINE=94283373; PubMed=8013449;			
RA	Toerrien A., Harkki A., Rouvinen J.;			
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from			
RT	Trichoderma reesei: two conformational states in the active site."			
RL	EMBO J. 13:2493-2501(1994).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).			
RC	STRAIN=C30;			
RX	MEDLINE=95127663; PubMed=7827044;			
RA	Toerrien A., Rouvinen J.;			
RT	"Structural comparison of two major endo-1,4-xylanases from			
RT	Trichoderma reesei."			
RL	Biochemistry 34:847-856(1995).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).			
RC	STRAIN=C30;			
RX	MEDLINE=96302263; PubMed=8755744;			
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.;			
RT	"Covalent binding of three epoxyalkyl xylosides to the active site of			
RT	endo-1,4-xylanase II from Trichoderma reesei."			
RL	Biochemistry 35:9617-9624(1996).			
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	-!- PATHWAY: Xylan degradation.			
CC	-!- PTM: THE N-TERMINUS IS BLOCKED.			
CC	-!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL			
CC	HYDROLASES).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			

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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; X69573; CAA49293.1; -  
DR PIR; S39154; S39154.  
DR PDB; 1XVO; 08-AUG-95.  
DR PDB; 1XVP; 08-AUG-95.  
DR PDB; 1ENX; 08-AUG-95.  
DR PDB; 1RED; 11-JAN-97.  
DR PDB; 1REE; 11-JAN-97.  
DR PDB; 1REF; 11-JAN-97.  
DR InterPro; IP001137; GH\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;  
KW 3D-structure.  
FT SIGNAL 1 32  
FT CHAIN 33 222 ENDO-1,4-BETA-XYLANASE 2.  
FT ACT\_SITE 118 118 NUCLEOPHILE.  
FT ACT\_SITE 209 209 PROTON DONOR.  
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;  
Best Local Similarity 100.0%; Pred. No. 2.8e-76;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNNNSGNSGNGVGGKQWPGTKNKVI 60  
DB 33 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNNNSGNSGNGVGGKQWPGTKNKVI 92  
QY 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFTGYNPSTGATKLGKGEVSDGSVDIYRT 120  
DB 93 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFTGYNPSTGATKLGKGEVSDGSVDIYRT 152  
QY 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180  
DB 153 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
DB 213 SSGSASITVS 222

RESULT 2  
XYN\_TRIHA STANDARD; PRT; 190 AA.  
AC P48793;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan  
DE xylanohydrolase).  
OS Trichoderma harzianum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreales; mitosporic Hypocreales; Trichoderma.  
OX NCBI\_TaxID=5544;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=E58;  
RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,  
RA Sessler J.N.  
RT "The amino acid sequence of the 20 kD xylanase from Trichoderma  
RT harzianum E58."  
RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,  
RL Voragen A.G.J. (eds.);

RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,  
RA Yaguchi M.;  
RT "High-resolution structures of xylanases from B.circulans and  
RT T.harzianum identify a new folding pattern and implications for the  
RT atomic basis of the catalysis."  
RL (In) Suominen P., Reinikainen T. (eds.);  
RL Trichoderma reesei cellulases and other hydrolases, pp.63-72.  
RL Foundation for Biotechnical and Industrial Fermentation Research,  
RL Helsinki (1993).  
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
CC linkages in xylans.  
CC -|- PATHWAY: Xylan degradation.  
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR PDB; 1XND; 20-DEC-94.  
DR InterPro; IP001137; GH\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.  
FT ACT\_SITE 86 86 NUCLEOPHILE.  
FT ACT\_SITE 177 177 PROTON DONOR.  
SQ SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;

Query Match 94.7%; Score 990; DB 1; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5.5e-72;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNNNSGNSGNGVGGKQWPGTKNKVI 60  
DB 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNNNSGNSGNGVGGKQWPGTKNKVI 60  
QY 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFTGYNPSTGATKLGKGEVSDGSVDIYRT 120  
DB 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFTGYNPSTGATKLGKGEVSDGSVDIYRT 120  
QY 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
XYNL\_EMENI STANDARD; PRT; 225 AA.  
AC P55332; Q00173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
DE (1,4-beta-D-xylan xylanohydrolase 1).  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=5072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96236210; PubMed=8787417;  
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;  
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two  
RT Aspergillus nidulans xylanase genes."  
RL Appl. Environ. Microbiol. 62:2179-2182(1996).  
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
CC linkages in xylans.  
CC -|- PATHWAY: Xylan degradation.  
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL



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CC HYDROLASES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z49892; CAA90073.1; -
CC HSP; P48793; IYND.
CC InterPro; IPR001137; GH_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC FT SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 225 ENDO-1,4-BETA-XYLANASE 1.
CC ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRC64;
CC -----
CC Query Match 65.5%; Score 684.5; DB 1; Length 225;
CC Best Local Similarity 66.1%; Pred. No. 1.2e-47;
CC Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;
CC -----
CC 7 TGYNNGFYSYWNDGCHGVYTYTNGGQFQSVNWSNFGVGGKQWOPCTKKNKVFSGSY 66
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 43 TGWNGYIYFQWTDGGDVTYTGAGGTYTQWNSNFGVGGKQWNPQS-TRTINYGGSF 101
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 67 NPNGNSLVYVWGRNPLIEYIIVENFTYNPSTGATKGLGVTSDGVSVDIYRTQRYNQ 126
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 102 NPSNGYLAVYGTQNPPLIEYIIVESYTYNPSSGGQHRGTVYSDGATYDIYATRYNAP 161
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 127 SIIGTATFYQVWSVRNRHSSGVSNTANHFNAWAOQGLTGLTMDYQIVAVEGYFSSGAS 186
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 162 SIETGATFQFWSVRQSKRTGTGTTTANHFNAWALGRLGTHNYQIVATEGYQSSGAS 221
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 187 ITV 189
CC |||
CC 222 ITV 224
CC -----
CC RESULT 4
CC XYNB_ASPAK
CC ID XYNB_ASPAK STANDARD; PRT; 225 AA.
CC AC P48824;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
CC DE (1,4-beta-D-xylan xylanohydrolase B).
CC GN XYNB.
CC OS Aspergillus awamori (var. kawachi).
CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
CC OX NCBI_TaxID=40384;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=IFO 4308;
CC RA Ito K.;
CC RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC CC -1- PATHWAY: Xylan degradation.
CC CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
CC EMBL; D38070; BAA07264.1; -
CC HSP; P36217; IXYO.
CC InterPro; IPR001137; GH_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC FT SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 225 ENDO-1,4-BETA-XYLANASE B.
CC ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;
CC -----
CC Query Match 64.7%; Score 676.5; DB 1; Length 225;
CC Best Local Similarity 66.1%; Pred. No. 5e-47;
CC Matches 121; Conservative 23; Mismatches 38; Indels 1; Gaps 1;
CC -----
CC 7 TGYNNGFYSYWNDGCHGVYTYTNGGQFQSVNWSNFGVGGKQWOPCTKKNKVFSGSY 66
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 43 TGENNGYIYFQWTDGGDVTYTGAGGTYTQWNSNFGVGGKQWNPQS-KDITYSGNF 101
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 67 NPNGNSLVYVWGRNPLIEYIIVENFTYNPSTGATKGLGVTSDGVSVDIYRTQRYNQ 126
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 102 TPSNGYLSVYGTWTDPLIEYIIVESYTYNPSSGGTTRGNSDGSVDIYATRYNAP 161
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 127 SIIGTATFYQVWSVRNRHSSGVSNTANHFNAWAOQGLTGLTMDYQIVAVEGYFSSGAS 186
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 162 SIQGTATFQVWSVRQSKRTGTGTTTANHFNAWALGRLGTHNYQIVATEGYQSSGSS 221
CC |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CC 187 ITV 189
CC |||
CC 222 ITI 224
CC -----
CC RESULT 5
CC XYN2_EMENI
CC ID XYN2_EMENI STANDARD; PRT; 221 AA.
CC AC P35333; Q00176;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2;
CC (1,4-beta-D-xylan xylanohydrolase 2)).
CC OS Emericella nidulans (Aspergillus nidulans).
CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC OC Eurotiales; Trichocomaceae; Emericella.
CC OX NCBI_TaxID=5072;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC MEDLINE=96236210; PubMed=8787417;
CC RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
CC RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
CC Aspergillus nidulans xylanase genes."
CC RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC CC -1- PATHWAY: Xylan degradation.
CC CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC EMBL; Z49893; CAA90074.1; -
DR HSSP; P48793; 1XND.
DR InterPro: IPR001137; GH.11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS; PRO0911; GLHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.
FT ACT_SITE 117 117 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 221 AA; 23517 MW; 4266E580DDE9475 CRC64;

Query Match 64.2%; Score 670.5; DB 1; Length 221;
Best Local Similarity 65.8%; Pred. No. 1.5e-46;
Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVINFGSGY 66
Db 39 TGTSGGYYSFMTDGGDVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVINFGSGY 66
QY 67 NPNGNSYLSVYGWNSRNPLEYIVENFGTYNPSTGATKLGCVTSVDSVYDIYRTQVNOP 126
Db 98 IPGNGYLSVYGWNSRNPLEYIVENFGTYNPSTGATKLGCVTSVDSVYDIYRTQVNOP 126
QY 127 SIIGTATFYQYWSVRNRHNSGNTANFNHNAWAQOGLTGTMDYQIVAVEGFSSGSAS 186
Db 158 SIIGTATFYQYWSVRNRHNSGNTANFNHNAWAQOGLTGTMDYQIVAVEGFSSGSAS 186
QY 187 ITVS 190
Db 218 ITVS 221

RESULT 6
XIN2_ASPNG STANDARD; PRT; 225 AA.
AC P55330; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; D38071; BAA07265.1; -
DR HSSP; P09850; 1XNB.
DR InterPro: IPR001137; GH.11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
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DR PRINTS; PRO0911; GLHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 37 ENDO-1,4-BETA-XYLANASE II.
FT CHAIN 121 225 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24057 MW; C4B8BB007AB2B8FD CRC64;

Query Match 63.6%; Score 664.5; DB 1; Length 225;
Best Local Similarity 65.6%; Pred. No. 4.4e-46;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVINFGSGY 66
Db 43 TGENNGFYYSFMTDGGDVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVINFGSGY 66
QY 67 NPNGNSYLSVYGWNSRNPLEYIVENFGTYNPSTGATKLGCVTSVDSVYDIYRTQVNOP 126
Db 102 TSGNGYLSVYGWNTDPLEIYIVESYGDYNGSGGTYKGTVDGSDVYDIYRTQVNOP 126
QY 127 SIIGTATFYQYWSVRNRHNSGNTANFNHNAWAQOGLTGTMDYQIVAVEGFSSGSAS 186
Db 162 SIIGTATFYQYWSVRNRHNSGNTANFNHNAWAQOGLTGTMDYQIVAVEGFSSGSAS 186
QY 187 ITV 189
Db 222 ITV 224

RESULT 7
XYNL_COCCA STANDARD; PRT; 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RX MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of xyl1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum.";
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -|- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- PTM: THE N-TERMINUS IS BLOCKED.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----

DR EMBL; L13596; AAA33024.1; -  
DR HSP; O43097; LYNA.  
DR InterPro: IPR001137; GH\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 221 ENDO-1,4-BETA-XYLANASE I.  
FT ACT\_SITE 115 115 NUCLEOPHILE (BY SIMILARITY).  
FT ACT\_SITE 206 206 PROTON DONOR (BY SIMILARITY).  
FT CONFLICT 81 81 W -> I (IN REF. 2).  
FT CONFLICT 107 107 G -> A (IN REF. 2).  
FT CONFLICT 131 131 S -> W (IN REF. 2).  
SQ SEQUENCE 221 AA; 23728 MW; 59DBD8983FC5B08C CRC64; ;

Query Match 62.2%; Score 650.5; DB 1; Length 221;  
Best Local Similarity 62.1%; Pred. No. 5.6e-45;  
Matches 118; Conservative 26; Mismatches 45; Indels 1; Gaps 1;  
QY 1 QTIQPGTYNGYFYSYWNDCGVTYTNPGGQFSYVNSNSGNGFVGKGWQPGTKNKVI 60  
Db 31 QNTPNGETHNGCFWNSDGGARATYTNAGAGSYYSWGGNVLGKGWNPCTA-RTI 89  
QY 61 NFGSYNPNGNSYLSVYWGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSYDIYRT 120  
Db 90 TYSCTYNGNSYLAVYWGTRNPLVEYIVENFGTYNPSTGATKLGVTSDGSYKIAQS 149  
QY 121 ORVNQPSITGATFYQYVSWVRNRHSSGVSNTANHFNAWAOQGLTLGTMQYQIVAVEGYF 180  
Db 150 TRTPNSIDGTRTFQYVSWVRNRHSSGVSNTANHFNAWAOQGLTLGTMQYQIVAVEGYF 209  
QY 181 SSGSASITVS 190  
Db 210 STGNAQITVN 219

RESULT 8  
XNA\_THELA  
ID XNA\_THELA STANDARD; PRT; 225 AA.  
AC O43097;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase).  
GN XNA.  
OS Thermomyces lanuginosus (Humicola lanuginosa).  
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.  
OX NCBI\_TaxID=5541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 5826 / Tsiklinsky;  
RA MEDLINE=97033440; PubMed=8879171;  
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;  
RT "Cloning and characterization of the gene for the thermostable  
xylanase xyna from Thermomyces lanuginosus.";  
RL J. Biotechnol. 49:211-218(1996).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).  
RC STRAIN=DSM 5826 / Tsiklinsky;  
RA MEDLINE=98426042; PubMed=9753433;  
RA Gruber K., Klintschar G., Hayn M., Schlacher A., Steiner W.,  
RA Kratky C.;  
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution  
X-ray structure and modeling studies.";  
RL Biochemistry 37:13475-13485(1998).

CC -!- FUNCTION: THERMOSTABLE XYLANASE.  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
CC linkages in xylans.  
CC -!- PATHWAY: Xylan degradation.  
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
CC -----

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CC -----

DR EMBL; U35436; AAB94633.1; -  
DR PDB; LYNA; 12-FEB-97  
DR InterPro: IPR001137; GH\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.  
FT SIGNAL 1 31  
FT CHAIN 32 225 ENDO-1,4-BETA-XYLANASE.  
FT ACT\_SITE 117 117 NUCLEOPHILE.  
FT ACT\_SITE 209 209 PROTON DONOR.  
FT MOD\_RES 32 32 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 141 185  
SQ SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 60.8%; Score 635.5; DB 1; Length 225;  
Best Local Similarity 60.2%; Pred. No. 8.9e-44;  
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;  
QY 1 QTIQPGTYNGYFYSYWNDCGVTYTNPGGQFSYVNSNSGNGFVGKGWQPGTKNKVI 60  
Db 32 QTPNSEGMDHGYYSWSDGGAQATYTNLEGTYEISWGGNVLGKGWNPGLNARAI 91  
QY 61 NFGSYNPNGNSYLSVYWGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSYDIYRT 120  
Db 92 HFEGYQPNNGNSYLAVYWGTRNPLVEYIVENFGTYNPSTGATKLGVTSDGSYLRGKT 151  
QY 121 ORVNQPSITGATFYQYVSWVRNRHSSGVSNTANHFNAWAOQGLTLGTMQYQIVAVEGY 179  
Db 152 TRVNAPSIDGTRTFQYVSWVRNRHSSGVSNTANHFNAWAOQGLTLGTMQYQIVAVEGY 211  
QY 180 FSSGSASITVS 190  
Db 212 FSSGYARITVA 222

RESULT 9  
XNLI\_HUMIN  
ID XNLI\_HUMIN STANDARD; PRT; 227 AA.  
AC P55334; Q12625;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
DE (1,4-beta-D-xylan xylanohydrolase 1).  
GN XYLI.  
OS Humicola insolens.  
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
OX NCBI\_TaxID=34413;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94247364; PubMed=8190078;  
RA Dalboege H., Hansen H.P.H.;  
RT "A novel method for efficient expression cloning of fungal enzyme  
genes.";  
RL Mol. Gen. Genet. 243:253-260(1994).  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

```

CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL; X76047; CAA53632.1; -
DR HSSP; Q43097; LYNA.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
KW SIGNAL 1 19
FT CHAIN 20 227
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCFEADALF CRC64;

Query Match 58.8%; Score 614.5; DB 1; Length 227;
Best Local Similarity 58.8%; Pred. No. 4.2e-42;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNGFYFYNDHGGVYITNGPGQFVSNMNSNGFVGGKQWPGTKNKVINFSGSYN 67
DB 44 GHNGFYFYSWSDGGQVQYTNLEGSRYQVRWNTGNFVGGKQWPGT-GRITNYGGYFN 102
QY 68 PGNNSVLSYGVNSRNPLEYIVENFTYNPSTGATKLGVEVSDGSDYDIYRTORVQPS 127
DB 103 PQNGGLAVGTWRNPLEYIVESTGTNPQSQAYKGTFTYDQYDIFVSTRYNQPS 162
QY 128 IGTATFYQVYVRRNHRSSGYSNTANHFNAWAQOGLTGLTMDYQIVAVEGYFSSGASI 187
DB 163 IDGTRFQYQWYSLRKNKRVGSGVNMNHFNAMQHQHMLQGHYQYVAVVEGYOSSGESDI 222
QY 188 TV 189
DB 223 YV 224

RESULT 10
ID XYNB_STRLI STANDARD; PRT; 335 AA.
AC P26515;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
GN (1,4-beta-D-xylan xylanhidrolase B).
GE XYNB.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteriales;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RL lividans."
RN Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 29-32 AND 252-307.
RC STRAIN=66 / 1326;

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RX MEDLINE=95189090; PubMed=7533741;
RA Shareck F., Biely P., Morosoli R., Kluepfel D.;
RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
RT reveals genes encoding acetyl xylan esterase and the RNA component of
RT ribonuclease P."
RL Gene 133:105-109(1995).
RN [3]
RP REVISION TO 225.
RA Shareck F.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE. THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS. XLYNA AND XLYNB SEEM TO ACT
CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLULOSE AND XULOSE
CC AS CARBON SOURCES.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL; M64552; AAC06114.2; -
DR HSSP; P09850; LXNB.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 41
FT CHAIN 42 335
FT DOMAIN 42 230 ENDO-1,4-BETA-XYLANASE B.
FT DOMAIN 231 249 CATALYTIC.
FT DOMAIN 250 335 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 250 335 XYLAN-BINDING (POTENTIAL).
FT ACT_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8F0CF CRC64;

Query Match 56.8%; Score 594; DB 1; Length 335;
Best Local Similarity 55.1%; Pred. No. 2.7e-40;
Matches 109; Conservative 32; Mismatches 41; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDHGGVYITNGPGQFVSNMNSNGFVGGKQW 52
DB 36 PGTAAQADTVTTTNOEGTNGNGYYSFWDTSQGTVSNMNSGGQYSTSWRTGNFVAGKGA 95
QY 53 PGTKNKVINFGSYNPNNGSYLSVYGVNSRNPLEYIVENFTYNPSTGATKLGVEVSDG 112
DB 96 NGGR-RTVQYSGSFNPSGNAYLALYGTWSNPLEYIVDNWGTYRP-TGEYK-GTVTSDG 152
QY 113 SYVDIYRTORVQPSIGTATGYQVYVRRNHRSSGYSNTANHFNAWAQOGLTGLTMD-Y 171
DB 153 GTYDIYKTRVKNKPSVEGTRTFDQYVSVKQSRKRTITGTGNHFDANARAGMPLGNFSY 212
QY 172 QIVAVEGYFSSGASITV 189
DB 213 MIMATEGYQSSGSSINV 230

RESULT 11
ID XYNB_STRLI STANDARD; PRT; 644 AA.
AC P54865;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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Db 159 ESTRVNOPSIEGRTTFOQYWAIRQQRKNSGTVNTGFFQAWERAGRMGNHNMIVATEG 218
QY 179 YFSSGSASITV 189
Db 219 YRSAGNSNINV 229

RESULT 13
XNLA_SCHCO STANDARD; PRT; 197 AA.
AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
  xylanohydrolase A).
GN XNLA.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.
RC STRAIN-ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
RL (in) Visser J., Beldman G., Kusters-van Someren M.A.,
RL Voragen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94063044; PubMed=8243636;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Jurasek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
  Schizophyllum commune.";
RT FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
  A from Schizophyllum commune.";
RL Eur. J. Biochem. 219:821-827(1994).
CC -|- FUNCTION: HYDROLYSES XYLANS INTO XYLOBIOSIOSE AND XYLOSE. THIS
  XYLANASE HAS A VERY BROAD PH ACTIVITY.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
  linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
  HYDROLASES).
DR PIR: S38973; S38973.
DR PIR: A44597; A44597.
DR HSP: Q43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;

Query Match 54.1%; Score 565.5; DB 1; Length 197;
Best Local Similarity 55.0%; Pred. No. 2.8e-38;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 7 TGVNGYFFSYWNDGGHYTYTNGQGFVNVNS-NSGNFVGKGWPGCTKNKNVNFSGS.65

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Db 7 TCTDGGYYTSMWTDGAGDATYQNNGGSTYTLTWSGNGNLVGGKWNPGAASSISYSGT 66
QY 66 YNPNGNSYLSVYGSWRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDYDVRTORVNO 125
Db 67 YQPNGNSYLSVYGVWTRSSLIIEYIVESYGSYDSSAASHKSGVTCNGATYDILSTWRYNA 126
QY 126 PSIGTATFYQYWSVRNRHRS-----SGSVNTANHFNAWAQQGLTLGT-MDYQIVAVEGY 179
Db 127 PSIDGTQTFEQFWSVRNPKKAPGSGISGTVQCHDFDANKGLGMNLGSEHNTQIVATEGY 186
QY 180 FSSGSASITVS 190
Db 187 QSSGTATITVT 197

RESULT 14
XNLC_STRLI STANDARD; PRT; 240 AA.
AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
  (1,4-beta-D-xylan xylanohydrolase C).
GN XLNC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
  lividans.";
RL Gene 107:75-82(1991).
CC -|- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
  COMPONENT OF PLANT CELL-WALLS.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
  linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
  HYDROLASES).
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  or send an email to license@isb-sib.ch)
  -----
DR EMBL: M64553; AAA26836.1; -.
DR EMBL: A25307; CAA01768.1; -.
DR PIR: JS0591; JS0591.
DR HSP: P09850; IXNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 50.4%; Score 527; DB 1; Length 240;
Best Local Similarity 53.1%; Pred. No. 3.9e-35;

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Matches 102; Conservative 30; Mismatches 50; Indels 10; Gaps 6;

Oy 2 TIQCTGYNNGYFYSYNDGHHGVTYNGPGQFVNNNSGNFVGGKGMOPGKTKNKVIN 61  
 Db 55 TNQGT---DGMYSFWTDGGGYSMTLNGGSGYSTQWTCNCFVAGKWSGTGDN--VR 109  
 Oy 62 FSGSYNPNNGSYLVYVWSRNPLEYIYVENFGTYNPSTGATKLGVEVTSVDSVYDIYRTQ 121  
 Db 110 YNGYFNPVNGYGLYGTWSPNLYEYIVDNNMGSYRP-TGYK-GTVSSDGGTVDIYQT 167  
 Oy 122 RVNPSIIGTATFYQYSVRNRHSSGS--VNTANHNANAAQGLTCTMD-YQIVAVEG 178  
 Db 168 RYNAPSVEGTFTFOQYWSVROSKVTSGTITTNHFDWARAGNMNQFRYYIMATEG 227  
 Oy 179 YFSSGSASITVS 190  
 Db 228 YQSSGSSNITVS 239

RESULT 15  
 XYNA\_BACST  
 ID XYNA\_BACST STANDARD; PRT; 210 AA.  
 AC P45705;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)  
 DE (1,4-beta-D-xylan xylanohydrolase A).  
 GN XYNA.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NO. 236;  
 RA Cho S., Choi Y.;  
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from  
 RT Bacillus stearothermophilus.";  
 RL J. Microbiol. Biotechnol. 5:117-124(1995).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN-NO. 236;  
 RA Cho S., Choi Y.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).

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EMBL; U15985; AAB72117.1;  
 HSSP; P09850; 1XNB.  
 InterPro; IPR001137; GH\_11.  
 Pfam; PF00457; Glyco\_hydro\_11; 1.  
 PRINTS; PR00911; GLHYDLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_Fil\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_Fil\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 19  
 FT CHAIN 20 210  
 FT ACT\_SITE 104 104  
 FT ACT\_SITE 197 197  
 FT ACT\_SITE 197 197  
 SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 50.3%; Score 525.5; DB 1; Length 210;

Best Local Similarity 54.1%; Pred. No. 4.4e-35;  
 Matches 98; Conservative 31; Mismatches 45; Indels 7; Gaps 5;

Oy 14 FYSYVNDGHHGVTYNGPGQFVNNNSGNFVGGKGMOPGKTKNKVIN-FSGSYNPNNGS 72  
 Db 31 YWQWTDDGGHVNNAVNGPGGNYSVTQNTGTFVVGKGMVTSVPRVINYAGIWEPSGNG 90  
 Oy 73 YLSYVGSNRNPLIEYIYVENFGTYNPSTGATKLGVEVTSVDSVYDIYRTQVNPSSIIGTA 132  
 Db 91 YLTLYGTRNALIEYIYVVDVDSWGTYP-TGNYK-GTVNSDGGTVDIYTTMRYNAPSIDGTQ 148  
 Oy 133 TFYQYWSYRRNHRSSG---SVNTANHNANAAQGLTLC-TMDYQIVAVEGFSSGSASIT 188  
 Db 149 TFQOFWSYRQSKRPTGSNVSTFNSHNVNANRSKGNLGSWAYQVLATGYQSSGRSNVT 208  
 Oy 189 V 189  
 Db 209 V 209

Search completed: May 9, 2003, 10:20:02  
 Job time : 26 secs

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OM protein - protein search, using sw model

Run on: May 9, 2003, 10:01:05 ; Search time 30 Seconds  
(without alignments)  
186.345 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGYNGYNGYFYWYND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	190	1	US-08-044-621D-26
2	1045	100.0	190	1	US-08-709-912-16
3	1045	100.0	190	2	US-09-047-370-16
4	1045	100.0	223	2	US-08-121-436A-2
5	1035	99.0	190	1	US-08-709-912-17
6	1035	99.0	190	2	US-09-047-370-17
7	1032	98.8	190	1	US-08-044-621D-27
8	1016	97.2	223	4	US-09-254-733-7
9	996	95.3	190	1	US-08-044-621D-28
10	996	95.3	190	1	US-08-709-912-14
11	996	95.3	190	2	US-09-047-370-14
12	721.5	69.0	261	4	US-08-768-373-2
13	665.5	63.7	225	1	US-08-290-979A-8
14	656.5	62.8	230	4	US-08-768-373-4
15	635.5	60.8	225	2	US-08-886-765-2
16	635.5	60.8	225	4	US-09-115-660-2
17	630	60.3	231	2	US-08-902-655A-6
18	630	60.3	296	3	US-08-507-431-6
19	630	60.3	296	3	US-09-116-622-6
20	630	60.3	296	4	US-09-219-277-6
21	630	60.3	296	4	US-09-599-661-6
22	620.5	59.4	227	1	US-08-458-023B-4
23	607.5	58.1	189	1	US-08-709-912-13
24	607.5	58.1	189	2	US-09-047-370-13
25	595.5	57.0	344	2	US-08-468-812-2
26	595.5	57.0	344	4	US-08-590-563-2
27	591	56.6	206	1	US-08-315-695-19

28	591	56.6	215	1	US-08-044-621D-34	Sequence 34, Appl
29	589	56.4	191	1	US-08-709-912-10	Sequence 10, Appl
30	589	56.4	191	2	US-09-047-370-10	Sequence 10, Appl
31	565.5	54.1	197	1	US-08-044-621D-29	Sequence 29, Appl
32	565.5	54.1	197	1	US-08-709-912-9	Sequence 9, Appl
33	565.5	54.1	197	2	US-09-047-370-9	Sequence 9, Appl
34	539.5	51.6	278	3	US-09-260-283-2	Sequence 2, Appl
35	530.5	50.8	211	1	US-08-575-964-1	Sequence 1, Appl
36	530.5	50.8	211	2	US-08-963-500-1	Sequence 1, Appl
37	529.5	50.7	189	1	US-08-044-621D-33	Sequence 33, Appl
38	528.5	50.6	368	3	US-08-591-685-13	Sequence 13, Appl
39	527.5	50.5	189	1	US-08-709-912-12	Sequence 12, Appl
40	527.5	50.5	189	2	US-09-047-370-12	Sequence 12, Appl
41	527	50.4	191	1	US-08-044-621D-35	Sequence 35, Appl
42	527	50.4	216	1	US-08-315-695-20	Sequence 20, Appl
43	526	50.3	200	1	US-07-744-570B-2	Sequence 2, Appl
44	525	50.2	191	1	US-08-709-912-11	Sequence 11, Appl
45	525	50.2	191	2	US-09-047-370-11	Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
; Sequence 26, Application US/08044621D  
; Patent No. 5405769  
; GENERAL INFORMATION:  
; APPLICANT: Warren W. Wakarchuk  
; APPLICANT: Wing L. Sung  
; APPLICANT: Makoto Yaguchi  
; APPLICANT: Robert L. Campbell  
; APPLICANT: David R. Rose  
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gowling, Strathy & Henderson  
; STREET: Suite 2600, 160 Elgin Street  
; CITY: Ottawa  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: K1P 1C3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 in., 360kB storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,621D  
; FILING DATE: April 8, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Judy A. Erratt  
; REGISTRATION NUMBER: 34,076  
; REFERENCE/DOCKET NUMBER: 08-863796  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 613-786-0199  
; TELEFAX: 613-563-9869  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 190  
; TYPE: Amino Acid  
; STRANDEDNESS: No. 5405769 Relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: protein  
; HYPOTHETICAL: No  
; ANTI-SENSE: No

```
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21kD, pi 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torionene, A., Mach, R. L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.
AUTHORS: & Kubicek, C. P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
DB 1 OTIQPTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
QY 61 NFSGSYNPNNGNSVLSYVWNSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGNSVLSYVWNSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
QY 121 QRYNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQQGLTLGTMQYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQQGLTLGTMQYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
; Sequence 16, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: xyn II
PUBLICATION INFORMATION:
AUTHORS: Torionene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
DB 1 OTIQPTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
QY 61 NFSGSYNPNNGNSVLSYVWNSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGNSVLSYVWNSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
QY 121 QRYNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQQGLTLGTMQYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNHRSSGVSNTANHFNAWAQQGLTLGTMQYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
; Sequence 16, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039,2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-09-047-370-16

Query Match 100.0%; Score 1045; DB 2; Length 190;  
Best Local Similarity 100.0%; Pred. No. 5e-90;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTQPTGTYNGYFYSYWNDGCHGVYTYTNGPGQFVSYNWNSNGNFVGGKQWPGTKNKVI 60  
Db 1 QTTQPTGTYNGYFYSYWNDGCHGVYTYTNGPGQFVSYNWNSNGNFVGGKQWPGTKNKVI 60  
QY 61 NFGSGYNPNNGNSYLSVYGWNRNPLIEYIIVENFGTYNPSTGATKGLGEVTSFGSVYDIYRT 120  
Db 61 NFGSGYNPNNGNSYLSVYGWNRNPLIEYIIVENFGTYNPSTGATKGLGEVTSFGSVYDIYRT 120  
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
Db 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 4

US-08-121-436A-2  
Sequence 2, Application US/08121436A  
Patent No. 5837515  
GENERAL INFORMATION:  
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
APPLICANT: Saarelainen, Ritva  
APPLICANT: Paloheimo, Marja  
APPLICANT: Lahtinen, Tarja  
APPLICANT: Fagerstr m, Richard  
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods  
TITLE OF INVENTION: for Their Production  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,436A  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,478  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI93/00221  
FILING DATE: 24-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,893  
FILING DATE: 29-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/524,308  
FILING DATE: 16-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimdala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.008000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-436A-2

Query Match 100.0%; Score 1045; DB 2; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6.1e-90;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTQPTGTYNGYFYSYWNDGCHGVYTYTNGPGQFVSYNWNSNGNFVGGKQWPGTKNKVI 60  
Db 34 QTTQPTGTYNGYFYSYWNDGCHGVYTYTNGPGQFVSYNWNSNGNFVGGKQWPGTKNKVI 93  
QY 61 NFGSGYNPNNGNSYLSVYGWNRNPLIEYIIVENFGTYNPSTGATKGLGEVTSFGSVYDIYRT 120  
Db 94 NFGSGYNPNNGNSYLSVYGWNRNPLIEYIIVENFGTYNPSTGATKGLGEVTSFGSVYDIYRT 153  
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180  
Db 154 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

## RESULT 5

US-08-709-912-17

```

Db      181 SSGSASITVS 190
|||||||
RESULT 6
US-09-047-370-17
; Sequence 17, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,912
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039,2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma viride
; PUBLICATION INFORMATION:
; AUTHORS: Yaguchi, M
; AUTHORS: Roy, C
; AUTHORS: Ujie, M
; AUTHORS: Watson, D. C.
; AUTHORS: Wakarchuk, W.
; JOURNAL: Xylan and Xylanase
; PAGES: 149-154
; DATE: 1992
US-09-047-370-17

```

```

; AUTHORS: raycchrl, M
;          Roy, C
; AUTHORS: Ujie, M
;          Watson, D. C.
; AUTHORS: Wakarchuk, W.
; JOURNAL: Xylan and Xylanase
; PAGES: 149-154
; DATE: 1992
US-09-047-370-17

Query Match      99.0%; Score 1035; DB 2; Length 190;
Best Local Similarity 98.9%; Pred. No. 4.3e-89;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OTTOPGTGYNNGYEPYSXWNDCHGGVTTNTPGGOFGSVNNNSGNFVGKGHPQTKNKVI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 OTIOPGTGFNNGYPYSXWNDCHGGVTTNTPGGOFGSVNNNSGNFVGKGHPQTKNKVI 60

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Qy 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120  
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180  
 Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180  
 Qy 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 7  
 US-08-044-621D-27  
 ; Sequence 27, Application US/08044621D  
 ; Patent No. 5405769  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warren W. Wakarchuk  
 ; APPLICANT: Wing L. Sung  
 ; APPLICANT: Makoto Yaguchi  
 ; APPLICANT: Robert L. Campbell  
 ; APPLICANT: David R. Rose  
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
 ; OF A LOW MOLECULAR MASS XYLANASE  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Gowling, Strathy & Henderson  
 ; STREET: Suite 2600, 160 Elgin Street  
 ; CITY: Ottawa  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: K1P 1C3  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/044.621D  
 ; FILING DATE: April 8, 1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Judy A. Erratt  
 ; REGISTRATION NUMBER: 34,076  
 ; REFERENCE/DOCKET NUMBER: 08-863796  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 613-786-0199  
 ; TELEFAX: 613-563-9869  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 190  
 ; TYPE: Amino Acid  
 ; STRANDEDNESS: No. 5405769 Relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; DESCRIPTION: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Trichoderma viride  
 ; STRAIN: Trichoderma viride, 20KD  
 ; IMMEDIATE SOURCE:  
 ; POSITION IN GENOME:  
 ; FEATURE:  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Yaguchi M., Roy C., Ujile M., Watson  
 ; AUTHORS: D.C., & Wakarchuk W.

; TITLE: Amino Acid Sequence of the Low-Molecular-  
 ; TITLE: Weight Xylanase from Trichoderma viride  
 ; JOURNAL: Xylans and Xylanases  
 ; VOLUME:  
 ; ISSUE:  
 ; PAGES: 149-154  
 ; DATE: 1992  
 ; DOCUMENT NUMBER:  
 ; FILING DATE:  
 ; PUBLICATION DATE:  
 ; RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-044-621D-27

Query Match 98.8%; Score 1032; DB 1; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 8.1e-89;  
 Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60  
 Db 1 QTIQPGTGFNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60  
 Qy 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120  
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180  
 Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180  
 Qy 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 8  
 US-09-254-733-7  
 ; Sequence 7, Application US/09254733  
 ; Patent No. 6277596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WATANABE, MANABU  
 ; APPLICANT: MORIYA, TATSUKI  
 ; APPLICANT: AOYAGI, KAORI  
 ; APPLICANT: SUMIDA, NAOMI  
 ; APPLICANT: MURAKAMI, TAKESHI  
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING  
 ; IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH  
 ; FILE REFERENCE: 99-0266\*/LC(WMC)/00144  
 ; CURRENT APPLICATION NUMBER: US/09/254.733  
 ; CURRENT FILING DATE: 1999-05-07  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1  
 US-09-254-733-7

Query Match 97.2%; Score 1016; DB 4; Length 223;  
 Best Local Similarity 96.8%; Pred. No. 3.1e-87;  
 Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60  
 Db 34 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 93  
 Qy 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120  
 Db 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 153  
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180  
 Db 154 QRVNPSIEGTSTFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 213



ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and xylanase  
PAGES: 435-438  
DATE: 1992  
US-08-709-912-14

Query Match 95.3%; Score 996; DB 1; Length 190;  
Best Local Similarity 94.7%; Pred. No. 1.8e-85;  
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 OTTQPTGTGNGYFYSYNDGCHGVYTYTNGPGQFVSNNNSGNGFVGGKQWQPGTKNKVI 60  
DB 1 OTTQPTGTGNGYFYSYNDGCHGVYTYTNGPGQFVSNNNSGNGFVGGKQWQPGTKNKVI 60  
QY 61 NFGSYNPNCGNSYLSVYWGSRNPLIEYIVENFGTNPSTGATKLGCVTSFGSVYDIYRT 120  
DB 61 NFGSYNPNCGNSYLSVYWGSRNPLIEYIVENFGTNPSTGATKLGCVTSFGSVYDIYRT 120  
QY 121 QRYNQPSIIIGTATFYQYWSVRRNRHSSGVSNTANHFNAMAQQGLTLGTMDYQIVAVEGYF 180  
DB 121 QRYNQPSIIIGTATFYQYWSVRRNRHSSGVSNTANHFNAMAQQGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 11

US-09-047-370-14  
Sequence 14, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of xylanase to improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and xylanase  
PAGES: 435-438  
DATE: 1992  
US-09-047-370-14

Query Match 95.3%; Score 996; DB 2; Length 190;  
Best Local Similarity 94.7%; Pred. No. 1.8e-85;  
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 OTTQPTGTGNGYFYSYNDGCHGVYTYTNGPGQFVSNNNSGNGFVGGKQWQPGTKNKVI 60  
DB 1 OTTQPTGTGNGYFYSYNDGCHGVYTYTNGPGQFVSNNNSGNGFVGGKQWQPGTKNKVI 60  
QY 61 NFGSYNPNCGNSYLSVYWGSRNPLIEYIVENFGTNPSTGATKLGCVTSFGSVYDIYRT 120  
DB 61 NFGSYNPNCGNSYLSVYWGSRNPLIEYIVENFGTNPSTGATKLGCVTSFGSVYDIYRT 120  
QY 121 QRYNQPSIIIGTATFYQYWSVRRNRHSSGVSNTANHFNAMAQQGLTLGTMDYQIVAVEGYF 180  
DB 121 QRYNQPSIIIGTATFYQYWSVRRNRHSSGVSNTANHFNAMAQQGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 12

US-08-768-373-2  
Sequence 2, Application US/08768373  
Patent No. 6228629  
GENERAL INFORMATION:  
APPLICANT: PALOHEIMO, MARJA  
APPLICANT: HAKOLA, SATU  
APPLICANT: M NYL, ARJA  
APPLICANT: VEHMAANPER, JARI  
APPLICANT: LANTTO, RAIJA  
APPLICANT: LAHTINEN, TARJA  
APPLICANT: FAGERSTR M, RICHARD  
APPLICANT: SUOMINEN, PIIRKO  
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```

RESULT 13
US-08-290-979A-8
; Sequence 8, Application US/08290979A
; Patent No. 5610046
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, Albert J.H.
; APPLICANT: DE GROAFF, Leendert H.
; APPLICANT: VAN DEN BROECK, Henriette C.
; APPLICANT: VISSER, Jacob
; TITLE OF INVENTION: Cloning and Expression of Xylanase B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812

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01 DB      102 TPGNGYLSVGYWTTDPLIEYYIVESYGDNPGSGGTYRGTVTSDGSVDIYTATFTNAA 161
02          :||| |||||||: ||| : | ||||||| |
03          :||| |||||||: ||| : | ||||||| |
04 QY      127 SIIGTATFYQWSVRNRHSSGVNTANHFNAWAQOGLTLGTMDYOIVA VEGVFSSGSAS 186
05          :||| |||||||: ||| : | ||||||| |
06 DB      162 SIOGTATFYQWSVRONKRVGGVTTSNHFNAWAKLGMNLGTHNYOIVATEGTOSSGSSS 221
07          :||| |||||||: ||| : | ||||||| |
08 QY      187 ITV 189
09          :|||
10 DB      222 ITV 224
11          :|||

RESULT l4
US-08-768-373-4
; Sequence 4 , Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NYTL , ARJA
; APPLICANT: VERMAANPER , JARI
; APPLICANT: LANTTO, RAIIA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: FAGERSTR M, RICHARD
; APPLICANT: SUOMINEN, PIIRKKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/768, 373  
;; FILING DATE: 17-DEC-1996  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/008, 746  
;; FILING DATE: 18-DEC-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/020, 839  
;; FILING DATE: 28-JUN-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CIMBALA, MICHELE A.  
;; REGISTRATION NUMBER: 33,851  
;; REFERENCE/DOCKET NUMBER: 1050.0540003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 230 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; ORGANISM: Chaetomium thermophilum  
;; STRAIN: CBS730.95  
;; FEATURE:  
;; NAME/KEY: Protein  
;; LOCATION: 1..230  
;; OTHER INFORMATION: /label= XLNB  
;; US-08-768-373-4

Query Match 62.8%; Score 656.5; DB 4; Length 230;  
Best Local Similarity 64.1%; Pred. No. 9.6e-54;  
Matches 118; Conservative 23; Mismatches 42; Indels 1; Gaps 1;  
Qy 6 GTGYNNGYFYSYNDGHGGVYTTNGPGQGFVSNNMSNGFVGGKGPQGTKNKVINFGSGS 65  
Db 45 GTGTHNGWYFSTWTDGGTGYWYTTNGNGSGSYNNQNGFVGGKGRWGAA-ATIKYSGN 103  
Qy .66 YNPNGNSYLSVYGSNRPLEYIYVENFGYNTNPSTGATKLGVEVTSVDSGVYDIYRTQVNO 125  
Db 104 YNPGNSYLAITGYTRNPLVEYIYVESYGYDPSGAQNLGTFQSDGQGYKIAKSTRYNA 163  
Qy 126 PSIIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWAQOGLTLGTMDYQIIVAVEGYFSSGSA 185  
Db 164 PSIEGKTFTQYWSVRSYKRVGGTGTVANHFNAWRSKGLNLGSHDYQIIVAVEGYKSSGSA 223  
Qy 186 SITV 189  
Db 224 SITV 227

RESULT 15  
US-08-886-765-2  
Sequence 2, Application US/08886765  
Patent No. 5817500  
GENERAL INFORMATION:  
APPLICANT: Hansen, Peter Kamp  
APPLICANT: Wagner, Peter  
APPLICANT: Mullertz, Anette  
APPLICANT: Knap, Inge Helmer  
TITLE OF INVENTION: Animal Feed Additives  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NO. 58175000 No. 5817500disk of No. 5817500th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/886, 765  
;; FILING DATE: 1-JUL-1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lambiris, Elias J  
;; REGISTRATION NUMBER: 33,728  
;; REFERENCE/DOCKET NUMBER: 4324.204-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-867-0123  
;; TELEFAX: 212-878-9655  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 225 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-886-765-2

Query Match 60.8%; Score 635.5; DB 2; Length 225;  
Best Local Similarity 60.2%; Pred. No. 8.4e-52;  
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;  
Qy 1 QTIQPGTGYNNGYFYSYNDGHGGVYTTNGPGQGFVSNNMSNGFVGGKGPQGTKNKVI 60  
Db 32 QTPNSEGWHGYYYSWSDGGAQATYINLEGGTYEISWGGNVLGGKGNPGLNARAI 91  
Qy 61 NFSGSYNPNNGNSYLSVYGSNRPLEYIYVENFGYNTNPSTGATKLGVEVTSVDSGVYDIYRT 120  
Db 92 HFEQVYQPNNGNSYLAIVYGTNRNPLVEYIYVENFGYDPSGATDLGTVECDGSIYRLGKT 151  
Qy 121 QRVNQPSIIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWAQOGLTL-GTMDYQIIVAVEGY 179  
Db 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDARAGLNVDGHDYIYQIVATEGY 211  
Qy 180 FSSGSASITVS 190  
Db 212 FSSGYARITVA 222

Search completed: May 9, 2003, 10:13:04  
Job time : 31 secs

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